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OM protein - protein search, using sw model

Run on: May 30, 2003, 09:49:41 ; Search time 22 seconds
(without alignments)
64.100 Million cell updates/sec

Title: SEQ1

Perfect score: 183

Sequence: 1 mcsnlstcvlgklsqelhkltqyprntgsgtpg 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	178	97.3	136	1	CAL1_ONCKE	P01263	oncorhynchu
2	159	86.9	32	1	CAL_ANGJA	P01262	anguilla ja
3	157	85.8	32	1	CAL2_ONCKE	P01264	oncorhynchu
4	157	85.8	138	1	CAL_CHICK	P07660	gallus gall
5	154	84.2	32	1	CAL3_ONCKI	P01265	oncorhynchu
6	108	59.0	136	1	CAL0_RAT	P01257	rattus norv
7	101	55.2	141	1	CAL0_HUMAN	P01258	homo sapien
8	100	54.6	136	1	CAL0_MOUSE	P01600	mus musculu
9	90	49.2	92	1	CAL_CANFA	P41547	canis famil
10	72	39.3	143	1	CAL_SHEEP	P01261	ovis aries
11	68	37.2	402	1	KPPR_SPIOL	P09559	spinacia ol
12	67	36.6	397	1	KPPR_MESCR	P27774	mesembryant
13	62	33.9	32	1	CAL_BOVIN	P01260	bos taurus
14	61	33.3	32	1	CAL_PIG	P01259	sus scrofa
15	61	33.3	395	1	KPPR_ARATH	P25697	arabidopsis
16	61	33.3	404	1	KPPR_WHEAT	P26302	triticum ae
17	54.5	29.8	213	1	NO2B_SOYEN	P08863	glycine max
18	54.5	29.8	401	1	SP2P_BACSU	P37968	bacillus su
19	52	28.4	375	1	KPPR_CHLRE	P19824	chlamydomon
20	51	27.9	491	1	AZAP_MOUSE	Q61247	mus musculu
21	49	26.8	400	1	EX7L_CLOPE	Q8xjd8	clostridium
22	49	26.8	529	1	EY98_HUMAN	Q9ulm2	homo sapien
23	49	26.8	939	1	EAE_ECO27	P19809	escherichia
24	48	26.8	3038	1	TRIO_HUMAN	O75962	homo sapien
25	48	26.2	180	1	REL5_SCHPO	Q09094	schizosacch
26	48	26.2	224	1	NUOB_BUCAL	P37253	buchnera ap
27	48	26.2	425	1	NG79_SCHPO	Q09793	schizosacch
28	48	26.2	747	1	YME1_YEAST	P32795	saccharomyc
29	48	26.2	1058	1	S185_YEAST	P40856	saccharomyc
30	47.5	26.0	1868	1	YHD0_YEAST	P38737	saccharomyc
31	47	25.7	240	1	IPT_AGRU4	P03869	agrobacteri
32	47	25.7	282	1	YQCD_ECOLI	Q46920	escherichia
33	47	25.7	391	1	Z072_XENLA	P18752	xenopus lae

34 47 25.7 474 1 MEC3_YEAST Q02574 saccharomyc
35 47 25.7 661 1 CA01_MOUSE Q9r0h0 mus musculu
36 47 25.7 661 1 CA01_RAT P07872 rattus norv
37 47 25.7 671 1 HPS4_MOUSE Q9kg97 mus musculu
38 47 25.7 1491 1 AT7A_MOUSE Q64430 mus musculu
39 47 25.7 1492 1 AT7A_RAT P70705 rattus norv
40 46.5 25.4 1916 1 RIF1_YEAST P29539 saccharomyc
41 46 25.1 245 1 Y542_CHLPN Q9z810 chlamydia p
42 46 25.1 262 1 APAL_BRARE O42363 brachydanio
43 46 25.1 332 1 KPPR_SVNY3 P37101 synchocyst
44 46 25.1 371 1 KLOM_EISFO O15991 eisenia foe
45 46 25.1 385 1 YDEM_ECOLI P76134 escherichia

ALIGNMENTS

RESULT 1
CAL1_ONCKE STANDARD; PRT; 136 AA.
AC P01263;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Calcitonin 1 precursor.
OS Oncorhynchus keta (Chum salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88083644; PubMed=3691820;
RA Poeschl E., Lindley I., Hofer E., Seifert J.M., Brunowsky W.,
RA Besemer J.;
RT "The structure of procalcitonin of the salmon as deduced from its
RT cDNA sequence.";
RL FEBS Lett. 226:96-100(1987).
RN [2]
RP SEQUENCE OF 85-116.
RX MEDLINE=70053602; PubMed=5261048;
RA Niall H.D., Keutmann H.T., Copp D.H., Potts J.T. Jr.;
RT "Amino acid sequence of salmon ultimobranchial calcitonin.";
Proc. Natl. Acad. Sci. U.S.A. 64:771-778(1969).
RN [3]
RP SYNTHESIS OF CALCITONIN.
RX MEDLINE=70067983; PubMed=5361911;
RA Guttman S., Pless J., Huguenin R.L., Sandrin E., Bossert H.,
RA Zehnder K.;
RT "Synthesis of salmon calcitonin, a high activity hypocalcemic
RT hormone.";
RL Helv. Chim. Acta 52:1789-1795(1969).
RN [4]
RP STRUCTURE BY NMR OF CALCITONIN.
RX MEDLINE=91120767; PubMed=1991104;
RA Meadows R.P., Nikonowicz E.P., Jones C.R., Bastian J.W.,
RA Gorenstein D.G.;
RT "Two-dimensional NMR and structure determination of salmon calcitonin
RT in methanol.";
RL Biochemistry 30:1247-1254(1991).
RN [5]
RP STRUCTURE BY NMR OF CALCITONIN.
RX MEDLINE=91255658; PubMed=2043752;
RA Meyer J.-P., Pelton J.T., Hoflack J., Saudek V.;
RT "Solution structure of salmon calcitonin.";
RL Biopolymers 31:233-241(1991).
RN [6]
RP STRUCTURE BY NMR OF CALCITONIN.
RX MEDLINE=92031485; PubMed=1931969;
RA Motta A., Pastore A., Goud N.A., Castiglione Morelli M.A.;
RT "Solution conformation of salmon calcitonin in sodium dodecyl sulfate
RT micelles as determined by two-dimensional NMR and distance geometry
RT calculations.";

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RL Biochemistry 30:10444-10450(1991).
CC -!- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
CC OF THOSE IONS IN THE BONES.
CC -!- PHARMACEUTICAL: Available under the names Calcimar (Rhône-Poulenc
CC Rorer), Miacalcin (Novartis) or Forcalcitonin (Unigene). Used for
CC the treatment of Paget's disease and hypercalcemia in malignancy.
CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
CC -----
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CC -----
CC EMBL: Y00765; CAA68734.1; ..
CC PIR: A01530; TCON
CC PIR: A31229; A31229.
CC HSSP: P01262; LBKU.
CC InterPro: IPR001693; Calcitonin-like.
CC InterPro: IPR001935; Calcitonin_A.
CC Pfam: PF00214; Calc_CGRP_IAPP; 1.
CC PRINTS: PR00270; CALCITONIN.
CC SMART: SM00113; CALCITONIN; 1.
CC PROSITE: PS00258; CALCITONIN; 1.
CC Cleavage on pair of basic residues; Amidation; Hormone; Signal;
KW Pharmaceutical.
FT SIGNAL 1 25 CALCITONIN 1.
FT PEPTIDE 83 114
FT DISULFID 83 89
FT MOD_RES 114 114
FT SEQUENCE 136 AA; 15179 MW; BDD867AE113B2A8 CRC64;

Query Match 97.3%; Score 178; DB 1; Length 136;
Best Local Similarity 100.08; Pred. No. 1.1e-18; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTGP 34
DB 83 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTGP 115

RESULT 2
CAL_ANGJA STANDARD; PRT; 32 AA.
AC P01262;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Calcitonin.
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=7937;
RN [1]
RP SEQUENCE.
RA Noda T., Narita K.;
RT "Amino acid sequence of eel calcitonin.";
RL J. Biochem. 79:353-359(1976).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=99315214; PubMed=10387083;
RA Hashimoto Y., Tona K., Nishikido J., Yamamoto K., Inazu T.,
RA Valentine K.G., Opella S.J.;
RT "Effects of glycosylation on the structure and dynamics of eel
RT calcitonin in micelles and lipid bilayers determined by nuclear
RT magnetic resonance spectroscopy.";
RL Biochemistry 38:8377-8384(1999).
CC -!- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION

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CC OF THOSE IONS IN THE BONES.
CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
CC PIR: A01529; TCPE.
CC PDB: 1BKU; 18-MAR-99.
CC InterPro: IPR001693; Calcitonin-like.
CC InterPro: IPR001935; Calcitonin_A.
CC Pfam: PF00214; Calc_CGRP_IAPP; 1.
CC PRINTS: PR00270; CALCITONIN.
CC SMART: SM00113; CALCITONIN; 1.
CC PROSITE: PS00258; CALCITONIN; 1.
CC Hormone; Amidation; 3D-structure.
KW Hormone; Amidation.
FT DISULFID 1 7
FT MOD_RES 32 32
FT SEQUENCE 32 AA; 3418 MW; AFC93549F8048922 CRC64;

Query Match 86.9%; Score 159; DB 1; Length 32;
Best Local Similarity 90.6%; Pred. No. 1.3e-16; Indels 0; Gaps 0;
Matches 29; Conservative 2; Mismatches 1;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTGP 33
DB 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTGP 32

RESULT 3
CAL2_ONCKE STANDARD; PRT; 32 AA.
ID CAL2_ONCKE
AC P01264;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Calcitonin 2.
OS Oncorhynchus keta (Chum salmon), and
OS Oncorhynchus nerka (Sockeye salmon), and
OS Oncorhynchus gorbuscha (Pink salmon) (Humpback salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018, 8023, 8017;
RN [1]
RP PRELIMINARY SEQUENCE.
RA Keutmann H.T., Lequin R.M., Habener J.F., Singer F.R., Niall H.D.,
RA Potts J.T. Jr.;
RT "Chemistry and physiology of the calcitonins: some recent advances.";
RL (In) Taylor S. (eds.);
RL Endocrinology 1971; proceedings of the third international symposium,
RL pp.316-323, Heinemann Medical Books, London (1972).
RN [2]
RP SYNTHESIS.
RX MEDLINE=73047885; PubMed=4508400;
RA Pless J., Bauer W., Bossert H., Zehnder K., Guttman S.;
RT "Synthesis of two natural salmon calcitonins.";
RL Nature New Biol. 240:62-63(1972).
CC -!- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
CC OF THOSE IONS IN THE BONES.
CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
CC PIR: C01531; TCON2C.
CC PIR: A01531; TCON2.
CC PIR: A01531; TCON2P.
CC HSSP: P01262; LBKU.
CC InterPro: IPR001693; Calcitonin-like.
CC InterPro: IPR001935; Calcitonin_A.
CC Pfam: PF00214; Calc_CGRP_IAPP; 1.
CC PRINTS: PR00270; CALCITONIN.
CC SMART: SM00113; CALCITONIN; 1.
CC PROSITE: PS00258; CALCITONIN; 1.
KW Hormone; Amidation.
FT DISULFID 1 7
FT MOD_RES 32 32
FT SEQUENCE 32 AA; 3387 MW; AFCB969AF807E7C2 CRC64;

Query Match 85.8%; Score 157; DB 1; Length 32;

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Query Match      84.2%; Score 154; DB 1; Length 32;
Best Local Similarity 84.4%; Pred. No. 6,7e-16;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 CSNLSVCVLGKLSQELHKLQTYPTNTGSGTP 33
    |||||:|||||:|||||:|||||:|||||:|
DB 1 CSNLSCTMLGKLSQDLHLKLTPTFTNTGAGVP 32
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RESULT 6
CALO_RAT
ID CALO_RAT STANDARD; PRT; 136 AA.
AC P01257;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcitonin precursor.
GN CALCA OR CALC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81225842; PubMed=6264603;
RA Jacobs J.W., Goodman R.H., Chin W.W., Dee P.C., Habener J.F.,
RA Bell N.H., Potts J.T. Jr.;
RT "Calcitonin messenger RNA encodes multiple polypeptides in a single
RT precursor."
RL Science 213:457-459(1981).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87025913; PubMed=6400492;
RA Rosenfeld M.G., Amara S.G., Evans R.M.;
RT "Alternative RNA processing events as a critical developmental
RT regulatory strategy in neuroendocrine gene expression."
RL Biochem. Soc. Symp. 49:27-44(1984).
RN [3]
RP SEQUENCE OF 83-136 FROM N.A.
RX MEDLINE=81054790; PubMed=6933496;
RA Amara S.G., David D.N., Rosenfeld M.G., Roos B.A., Evans R.M.;
RT "Characterization of rat calcitonin mRNA."
RL Proc. Natl. Acad. Sci. U.S.A. 77:4444-4448(1980).
RN [4]
RP SEQUENCE OF 85-116.
RX MEDLINE=76210265; PubMed=12781175;
RA Raulais D., Hagaman J., Ontjes D.A., Lundblad R.L., Kingdon H.S.;
RT "The complete amino-acid sequence of rat thyrocalcitonin."
RL Eur. J. Biochem. 64:607-611(1976).
CC -1- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
CC OF THOSE IONS IN THE BONES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS: THE CALCITONIN PRECURSOR AND THE CALCITONIN
CC RELATED PEPTIDE PRECURSOR ARE OBTAINED BY TISSUE-SPECIFIC SPLICING
CC OF THE SAME GENE.
CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
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CC EMBL; V01230; CAA24540.1; -
CC EMBL; V01228; CAA24538.1; -
CC EMBL; V01223; CAA24539.1; -
CC EMBL; M26137; AAA40849.1; -
CC EMBL; M31027; AAB59681.1; -
CC EMBL; L00109; AAB59681.1; JOINED.
CC EMBL; L00110; AAB59681.1; JOINED.
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PIR; A01525; TCRT.
DR HSP; P01262; IBRU.
DR InterPro; IPR001693; Calcitonin-like.
DR InterPro; IPR001935; Calcitonin_A.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00270; CALCITONIN_A.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
KW Cleavage on pair of basic residues; Signal; Amidation; Hormone;
KW Glycoprotein; Alternative splicing.
FT SIGNAL 1 25
FT PROPEP 26 82
FT PEPTIDE 85 116
FT PROPEP 121 136
FT DISULFID 85 91
FT CARBOHYD 87 87
FT MOD_RES 116 116
FT SEQUENCE 136 AA; 15103 MW; A197358A802222F7 CRC64;
Query Match 59.0%; Score 108; DB 1; Length 136;
Best Local Similarity 54.5%; Pred. No. 1.4e-08;
Matches 18; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 CSNLSCTVLGKLSQELHKLQTYPTNTGSGTPG 34
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DB 85 CGNLSCTMLGTYTDLNKFHTFPQTSGVGAPG 117
    |||||:|:|:|:|:|:|:|:|:|

RESULT 7
CALO_HUMAN
ID CALO_HUMAN STANDARD; PRT; 141 AA.
AC P01258; Q13937;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcitonin precursor [Contains: Calcitonin; Katacalcin (Calcitonin
DE carboxyl-terminal peptide) (CCP) (PDN-21)].
GN CALCA OR CALCI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=89386053; PubMed=25711128;
RA Broad P.M., Symes A.J., Thakker R.V., Craig R.K.;
RT "Structure and methylation of the human calcitonin/alpha-CGRP gene."
RL Nucleic Acids Res. 17:6999-7011(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=84132556; PubMed=6546550;
RA le Moulec J.M., Jullienne A., Chenais J., Lasmoles F.,
RA Gullana J.M., Milhaud G., Moukhtar M.S.;
RT "The complete sequence of human preprocalcitonin."
RL FEBS Lett. 167:93-97(1984).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=85166259; PubMed=3872459;
RA Jonas V., Lin C.R., Kawashima E., Semon D., Swanson L.W.,
RA Mermod J.-J., Evans R.M., Rosenfeld M.G.;
RT "Alternative RNA processing events in human calcitonin/calcitonin
RT gene-related peptide gene expression."
RL Proc. Natl. Acad. Sci. U.S.A. 82:1994-1998(1985).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=86164952; PubMed=3485540;
RA Riley J.H., Edbrooke M.R., Craig R.K.;
RT "Ectopic synthesis of high-Mr calcitonin by the BEN lung carcinoma
RT cell line reflects aberrant proteolytic processing."
RL FEBS Lett. 198:71-79(1986).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=87213363; PubMed=3034287;
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RA Craig R.K., Riley J.H., Edbrooke M.R., Broad P.M., Poord S.M.,
RA Al-Kazwini S.J., Holman J.J., Marshall I.,
RT "Expression and function of the human calcitonin/alpha-CGRP gene in
RL health and disease."
RL Biochem. Soc. Symp. 52:91-105(1986).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Thyroid carcinoma;
RX MEDLINE=92105127; PubMed=1761559;
RA Minvielle S., Giscard-Dartevelle S., Cohen R., Taboulet J., Iabaye F.,
RA Julienne A., Rivaille P., Milhaud G., Moukhtar M.S., Lasmoules F.,
RT "A novel calcitonin carboxyl-terminal peptide produced in medullary
RT thyroid carcinoma by alternative RNA processing of the
RL calcitonin/calcitonin gene-related peptide gene."
RL J. Biol. Chem. 266:24627-24631(1991).
RN [7]
RP SEQUENCE OF 49-141 FROM N.A. (ISOFORM 1).
RX MEDLINE=85230541; PubMed=2408883;
RA Edbrooke M.R., Parker D., McVey J.H., Riley J.H., Sorenson G.D.,
RA Pettengill O.S., Craig R.K.,
RT "Expression of the human calcitonin/CGRP gene in lung and thyroid
RT carcinoma."
RL EMBO J. 4:715-724(1985).
RN [8]
RP SEQUENCE OF 48-83 FROM N.A.
RX MEDLINE=85022523; PubMed=6148938;
RA Nelkin B.D., Rosenfeld K.I., de Bustros A., Leong S.S., Roos B.A.,
RA Baylin S.B.,
RT "Structure and expression of a gene encoding human calcitonin and
RT calcitonin gene related peptide."
RL Biochem. Biophys. Res. Commun. 123:648-655(1984).
RN [9]
RP SEQUENCE OF 85-116.
RX MEDLINE=72162720; PubMed=5760861;
RA Neher R., Riniker B., Rittel W., Zuber H.,
RA "Human calcitonin. Structure of calcitonin M and D."
RL Helv. Chim. Acta 51:1900-1905(1968).
RN [10]
RP STRUCTURE BY NMR OF CALCITONIN.
RX MEDLINE=91159414; PubMed=2001366;
RA Motta A., Temussi P.A., Wunsch E., Bovermann G.,
RT "A 1H NMR study of human calcitonin in solution."
RL Biochemistry 30:2364-2371(1991).
RN [11]
RP CHARACTERIZATION OF KATACALCIN.
RX MEDLINE=83166029; PubMed=6132180;
RA Hillyard C.J., Myers C., Abeyasekera G., Steverson J.C.,
RA Craig R.K., MacIntyre I.,
RT "Katacalcine: a new plasma calcium-lowering hormone."
RL Lancet 1:846-848(1983).
CC -!- FUNCTION: CALCITONIN CAUSES A RAPID BUT SHORT-LIVED DROP IN THE
CC LEVEL OF CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE
CC INCORPORATION OF THOSE IONS IN THE BONES.
CC -!- FUNCTION: Katacalcine is a potent plasma calcium-lowering peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC P06881; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3 (AC
CC P06881); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
CC -----
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CC -----
DR EMBL; X15943; CAA34070.1; ALT_SEQ.
DR EMBL; X00356; CAA25103.1;
DR EMBL; K03513; AAA52124.1;
DR EMBL; M12666; AAA51913.1;
DR EMBL; M12664; AAA51913.1; JOINED.
DR EMBL; M12665; AAA51913.1; JOINED.

DR EMBL; X03662; CAA27299.1;
DR EMBL; M64486; AAA58403.1;
DR EMBL; M26095; AAA35501.1;
DR PIR; A22716; TCHU.
DR PIR; C22949; C22949.
DR PIR; S07238; S07238.
DR PIR; S07242; S07242.
DR PIR; S07643; S07643.
DR HSSP; P01262; 1BKU.
DR Genew; HGNC:1437; CALCA.
DR MIM; 114130;
DR InterPro; IPR001693; Calcitonin-like.
DR InterPro; IPR001935; Calcitonin A.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00270; CALCITONIN.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
KW Cleavage on pair of basic residues; Amidation; Alternative splicing;
KW Hormone; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT PROPEP 26 82
FT PEPTIDE 85 116 CALCITONIN.
FT PEPTIDE 121 141 KATACALCIN.
FT DISULFID 85 91
FT MOD_RES 116 116
FT VARSPIC 134 141
FT CONFLICT 92 92
SQ SEQUENCE 141 AA; 15467 MW; 99622305DD8B286F CRC64;
Query Match 55.2%; Score 101; DB 1; Length 141;
Best Local Similarity 51.5%; Pred. No. 1.5e-07;
Matches 17; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
QY 2 CSNLSTCVLGLKLSOELHKLQTYPRNTGSGTPG 34
DB 85 CGNLSTCMGLTYTQDFNKFHTFPQTATGVGAPG 117

RESULT 8
CALO_MOUSE
ID CALO_MOUSE STANDARD; PRT; 136 AA.
AC P70160;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcitonin precursor.
GN CALCA OR CALC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid;
RX MEDLINE=96400274; PubMed=8806650;
RA Rehli M., Luger K., Beier W., Falk W.,
RT "Molecular cloning and expression of mouse procalcitonin."
RL Biochem. Biophys. Res. Commun. 226:420-425(1996).
CC -!- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
CC OF THOSE IONS IN THE BONES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2 (AC
CC Q95JAO); are produced by alternative splicing.
CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
CC -----
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CC -----

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CC EMBL; X97991; CAA66630.1;
DR HSSP; P01262; 1BKU.
DR MGD; MG1:2151253; Calca.
DR InterPro; IPR001693; Calcitonin-like.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00270; CALCITONIN_A.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
KW Cleavage on pair of basic residues; Signal; Amidation; Hormone;
KW Glycoprotein; Alternative splicing.
FT SIGNAL 1 25
FT PROPEP 26 82
FT PEPTIDE 85 116
FT PROPEP 121 136
FT DISULFID 85 91
FT CARBOHYD 87 87
FT MOD_RES 116 116
FT SEQUENCE 136 AA; 15141 MW; B7F1DD27F7E10DE5 CRC64;
SQ
Query Match 54.6%; Score 100; DB 1; Length 136;
Best Local Similarity 51.5%; Pred. No. 2.1e-07;
Matches 17; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34
DB 85 CGNLSTCMGLTGTQDLNKFHTFPQTSIGVEAPG 117
RESULT 9
CALCANFA
ID CALCANFA STANDARD; PRT; 92 AA.
AC P41547;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcitonin precursor (Fragments).
GN CALC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE OF 1-25, AND SEQUENCE OF 26-92 FROM N.A.
RX MEDLINE=92100867; PubMed=1758974;
RA Mel J.A., Kwant M.M., Arnold I.C.J., Hazewinkel H.A.W.;
RT "Elucidation of the sequence of canine (pro)-calcitonin. A molecular
RL Regul. Pept. 35:189-195(1991).
CC -1- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
CC OF THOSE IONS IN THE BONES.
CC -1- TISSUE SPECIFICITY: SYNTHESIZED BY C-CELLS OF THE THYROID GLAND.
CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
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-----
CC EMBL; X56994; CAA40311.1; ALT_SEQ.
DR HSSP; P01262; 1BKU.
DR InterPro; IPR001693; Calcitonin-like.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00270; CALCITONIN_A.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
-----
KW Hormone; Amidation; Cleavage on pair of basic residues.
FT NON_CONS 25 26
FT PEPTIDE 47 78
FT DISULFID 47 53
FT MOD_RES 78 78
FT SEQUENCE 92 AA; 9974 MW; 53B103230864039D CRC64;
SQ
Query Match 49.28; Score 90; DB 1; Length 92;
Best Local Similarity 51.5%; Pred. No. 3.8e-06;
Matches 17; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34
DB 47 CSNLSTCVLGTSKDLNFFHFGSIGFGAETPG 79
RESULT 10
CAL_SHEEP
ID CAL_SHEEP STANDARD; PRT; 143 AA.
AC P01261;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcitonin precursor.
GN CT.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93246256; PubMed=8482543;
RA Kumaraswamy A., Borges M., Tamir H., Nelkin B.D.;
RT "Cloning of a cDNA encoding sheep calcitonin from a thyroid C-cell
RN library."
RL Gene 126:269-273(1993).
RN [2]
RP SEQUENCE OF 87-118.
RA Sauer R., Niall H.D., Potts J.T. Jr.;
RT "Accelerated procedures for automated peptide degradation."
RL Fed. Proc. 29:728-728(1970).
CC -1- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
CC OF THOSE IONS IN THE BONES.
CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
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CC EMBL; M98053; -; NOT_ANNOTATED_CDS.
DR PIR; JN0580; TCSH.
DR InterPro; IPR001693; Calcitonin-like.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00270; CALCITONIN_A.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
KW Cleavage on pair of basic residues; Amidation; Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 84
FT PEPTIDE 87 118
FT PROPEP 122 143
FT DISULFID 87 93
FT MOD_RES 118 118
AMIDATION (G-119 PROVIDE AMIDE GROUP).
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KW Hormone; Amidation; Cleavage on pair of basic residues.
FT NON_CONS 25 26
FT PEPTIDE 47 78
FT DISULFID 47 53
FT MOD_RES 78 78
FT SEQUENCE 92 AA; 9974 MW; 53B103230864039D CRC64;
SQ
Query Match 49.28; Score 90; DB 1; Length 92;
Best Local Similarity 51.5%; Pred. No. 3.8e-06;
Matches 17; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34
DB 47 CSNLSTCVLGTSKDLNFFHFGSIGFGAETPG 79
RESULT 10
CAL_SHEEP
ID CAL_SHEEP STANDARD; PRT; 143 AA.
AC P01261;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcitonin precursor.
GN CT.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93246256; PubMed=8482543;
RA Kumaraswamy A., Borges M., Tamir H., Nelkin B.D.;
RT "Cloning of a cDNA encoding sheep calcitonin from a thyroid C-cell
RN library."
RL Gene 126:269-273(1993).
RN [2]
RP SEQUENCE OF 87-118.
RA Sauer R., Niall H.D., Potts J.T. Jr.;
RT "Accelerated procedures for automated peptide degradation."
RL Fed. Proc. 29:728-728(1970).
CC -1- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
CC OF THOSE IONS IN THE BONES.
CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
-----
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-----
CC EMBL; M98053; -; NOT_ANNOTATED_CDS.
DR PIR; JN0580; TCSH.
DR InterPro; IPR001693; Calcitonin-like.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00270; CALCITONIN_A.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
KW Cleavage on pair of basic residues; Amidation; Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 84
FT PEPTIDE 87 118
FT PROPEP 122 143
FT DISULFID 87 93
FT MOD_RES 118 118
AMIDATION (G-119 PROVIDE AMIDE GROUP).
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SQ SEQUENCE 143 AA; 15658 MW; D4CEB15C5C06B663 CRC64;
Query Match 39.3%; Score 72; DB 1; Length 143;
Best Local Similarity 45.5%; Pred. No. 0.0024;
Matches 15; Conservative 3; Mismatches 15; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTGP 34
||||| :|: | | |
DB 87 CSNLSTCVLSAYWKDLNNYHRYSGMGFGPETGP 119

RESULT 11
KPPR_SPIOI STANDARD; PRT; 402 AA.
AC P09559;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphoribulokinase, chloroplast precursor (EC 2.7.1.19)
DE (Phosphopentokinase) (PRKASE) (PRK).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88303351; PubMed=2841650;
RA Roesler K.R., Ogren W.L.;
RT "Nucleotide sequence of spinach cDNA encoding phosphoribulokinase.";
RL Nucleic Acids Res. 16:7192-7192(1988).
RN [2]
RP SEQUENCE OF 7-402 FROM N.A.
RX MEDLINE=88329728; PubMed=2843430;
RA Milanez S., Mural R.J.;
RT "Cloning and sequencing of cDNA encoding the mature form of
RT phosphoribulokinase from spinach.";
RL Gene 66:55-63(1988).
RN [3]
RP SEQUENCE OF 52-69.
RX MEDLINE=86129440; PubMed=3004354;
RA Porter M.A., Milanez S., Stringer C.D., Hartman F.C.;
RT "Purification and characterization of ribulose-5-phosphate kinase
RT from spinach.";
RL Arch. Biochem. Biophys. 245:14-23(1986).
RN [4]
RP SEQUENCE OF 52-69.
RA Porter M.A., Hartman F.C.;
RT "Commonality of catalytic and regulatory sites of spinach
RT phosphoribulokinase: Characterization of a tryptic peptide that
RT contains an essential cysteinyl residue.";
RL Biochemistry 25:7314-7318(1986).
RN [5]
RP DISULFIDE BOND, AND PARTIAL SEQUENCE.
RX MEDLINE=88087076; PubMed=2826432;
RA Porter M.A., Stringer C.D., Hartman F.C.;
RT "Characterization of the regulatory thioredoxin site of
RT phosphoribulokinase.";
RL J. Biol. Chem. 263:123-129(1988).
CC -!- CATALYTIC ACTIVITY: ATP + D-ribulose 5-phosphate = ADP + D-
CC ribulose 1,5-bisphosphate.
CC -!- ENZYME REGULATION: LIGHT REGULATED VIA THIOREDOXIN BY REVERSIBLE
CC OXIDATION/REDUCTION OF SULFHYDRYL/DISULFIDE GROUPS.
CC -!- PATHWAY: Calvin cycle.
CC -!- SIMILARITY: BELONGS TO THE PHOSPHORIBULOKINASE FAMILY.
CC
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CC
CC EMBL; M73707; AAA33034.1;
CC InterPro; IPR001324; PRK.
CC Pfam; PF00485; PRK; 1.
CC PRINTS; PR00478; PHRIBLKINASE.
CC PROSITE; PS00567; PHOSPHORIBULOKINASE; 1.
CC Transferase; Kinase; Chloroplast; Transit peptide; Calvin cycle;
CC ATP-binding; Photosynthesis.
CC ATP-binding; Photosynthesis.
CC TRANSIT 1 44
CC CHAIN 45 397
CC DISULFID 62 101
CC SEQUENCE 397 AA; 44114 MW; 88DC418E211EC975 CRC64;
Query Match 36.6%; Score 67; DB 1; Length 397;

CC EMBL; X07654; CAA30499.1;
CC EMBL; M21338; AAA34036.1; ALT_INIT.
CC PIR; A25182; A25182.
CC PIR; A25250; A25250.
CC PIR; JA0064; JA0064.
CC PIR; S02099; S02099.
CC InterPro; IPR001324; PRK.
CC Pfam; PF00485; PRK; 1.
CC PRINTS; PR00478; PHRIBLKINASE.
CC PROSITE; PS00567; PHOSPHORIBULOKINASE; 1.
CC Transferase; Kinase; Chloroplast; Transit peptide; Calvin cycle;
CC ATP-binding; Photosynthesis.
CC TRANSIT 1 51
CC CHAIN 52 402
CC DISULFID 67 106
CC SEQUENCE 402 AA; 45007 MW; 450759B96A675C6B CRC64;
Query Match 37.2%; Score 68; DB 1; Length 402;
Best Local Similarity 44.8%; Pred. No. 0.028;
Matches 13; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 3 SNLSTCVLGKLSQELHKLQTYPRNTGSG 31
||||| :|: | | |
DB 343 SNLSTKFEYGEVTQQLRHQNFPGSNNGTG 371

RESULT 12
KPPR_MESCR STANDARD; PRT; 397 AA.
AC P27774;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphoribulokinase, chloroplast precursor (EC 2.7.1.19)
DE (Phosphopentokinase) (PRKASE) (PRK).
OS Mesembryanthemum crystallinum (Common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
OX NCBI_TaxID=3544;
RN [1]
RP SEQUENCE FROM N.A.
RX Michalowski C.B., Derocher E.J., Bohnert H.J., Salvucci M.E.;
RT Submitted (XXX-1991) to the EMBL/GenBank/DBJ databases.
RL -!- CATALYTIC ACTIVITY: ATP + D-ribulose 5-phosphate = ADP + D-
RL ribulose 1,5-bisphosphate.
RL -!- ENZYME REGULATION: LIGHT REGULATED VIA THIOREDOXIN BY REVERSIBLE
RL OXIDATION/REDUCTION OF SULFHYDRYL/DISULFIDE GROUPS.
RL -!- PATHWAY: Calvin cycle.
RL -!- SIMILARITY: BELONGS TO THE PHOSPHORIBULOKINASE FAMILY.
RL
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RL
RL EMBL; M73707; AAA33034.1;
RL InterPro; IPR001324; PRK.
RL Pfam; PF00485; PRK; 1.
RL PRINTS; PR00478; PHRIBLKINASE.
RL PROSITE; PS00567; PHOSPHORIBULOKINASE; 1.
RL Transferase; Kinase; Chloroplast; Transit peptide; Calvin cycle;
RL ATP-binding; Photosynthesis.
RL TRANSIT 1 44
RL CHAIN 45 397
RL DISULFID 62 101
RL SEQUENCE 397 AA; 44114 MW; 88DC418E211EC975 CRC64;
Query Match 36.6%; Score 67; DB 1; Length 397;
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Best Local Similarity 44.8%; Pred. No. 0.039;
Matches 13; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 3 SNLSTCVLKGKLSQELHKLQTYPTNTGSG 31
||||| |:|:|:| |:|:|:|
DB 338 SNLSTKFGYEVTOQLMKHQDFPGSNGTG 366

RESULT 13
CAL_BOVIN
ID CAL_BOVIN STANDARD; PRT; 32 AA.
AC P01260;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Calcitonin.
GN CALC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=70025647; PubMed=5259773;
RA Brewer H.B. Jr., Ronan R.;
RT "Amino acid sequence of bovine thyrocalcitonin.";
RL Proc. Natl. Acad. Sci. U.S.A. 63:940-947(1969).
CC -!- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
CC OF THOSE IONS IN THE BONES.
CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
DR PIR: A01528; TCBO.
DR InterPro: IPR001693; Calcitonin-like.
DR InterPro: IPR001935; Calcitonin_A.
DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS: PR00270; CALCITONIN.
DR SMART: SM00113; CALCITONIN; 1.
DR PROSITE: PS00258; CALCITONIN; 1.
KW Hormone; Amidation.
FT DISULFID 1
FT MOD_RES 32 32
SQ SEQUENCE 32 AA; 3596 MW; EDEA2A3ADFFE4909 CRC64;

Query Match 33.9%; Score 62; DB 1; Length 32;
Best Local Similarity 40.6%; Pred. No. 0.013;
Matches 13; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

QY 2 CSNLSTCVLKGKLSQELHKLQTYPTNTGSGTP 33
||||| |:|:|:| |:|:|:|
DB 1 CSNLSTCVLSAYWKDLNLYHRFSGMGFGPETP 32

RESULT 14
CAL_PIG
ID CAL_PIG STANDARD; PRT; 32 AA.
AC P01259;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Calcitonin.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=68270618; PubMed=5240032;
RA Potts J.T. Jr., Niall H.D., Keutmann H.T., Brewer H.B. Jr.,
RA Defotis L.J.;
RT "The amino acid sequence of porcine thyrocalcitonin.";
RL Proc. Natl. Acad. Sci. U.S.A. 59:1321-1328(1968).
RN [2]

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RP SEQUENCE.
RX MEDLINE=70161016; PubMed=5462122;
RA Barg W.F. Jr., Englert M.E., Davies M.C., Colucci D.F., Snedeker E.H.,
RA Dziobkowski C., Bell P.H.;
RT "Degradation and structure of porcine calcitonin-1.";
RL Biochemistry 9:1671-1676(1970).
RN [3]
RP SEQUENCE.
RX MEDLINE=69012693; PubMed=5693288;
RA Neher R., Riniker B., Zuber H., Rittel W., Kahnt F.W.;
RT "Thyrocalcitonin. II. Structure of alpha-thyrocalcitonin.";
RL Helv. Chim. Acta 51:917-924(1968).
CC -!- FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL OF
CC CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE INCORPORATION
CC OF THOSE IONS IN THE BONES.
CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
DR PIR: A01527; TCGP.
DR InterPro: IPR001693; Calcitonin-like.
DR InterPro: IPR001935; Calcitonin_A.
DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS: PR00270; CALCITONIN.
DR SMART: SM00113; CALCITONIN; 1.
DR PROSITE: PS00258; CALCITONIN; 1.
KW Hormone; Amidation.
FT DISULFID 1
FT MOD_RES 32 32
SQ SEQUENCE 32 AA; 3607 MW; EDE755ED2FE6EA09 CRC64;

Query Match 33.3%; Score 61; DB 1; Length 32;
Best Local Similarity 40.6%; Pred. No. 0.018;
Matches 13; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

QY 2 CSNLSTCVLKGKLSQELHKLQTYPTNTGSGTP 33
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DB 1 CSNLSTCVLSAYWRNLNHFSGMGFGPETP 32

RESULT 15
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ID KPPR_ARATH STANDARD; PRT; 395 AA.
AC P25697;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphoribulokinase, chloroplast precursor (EC 2.7.1.19)
DE (Phosphopentokinase) (PRKASE) (PRK).
GN AT1G32060 OR t12021.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. C24;
RX MEDLINE=91329732; PubMed=1651130;
RA Horsnell P.R., Raines C.A.;
RT "Nucleotide sequence of a cDNA clone encoding chloroplast
RT phosphoribulokinase from Arabidopsis thaliana.";
RL Plant Mol. Biol. 17:183-184(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

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RA Lin X., Liu Z.X., Liu Z.A., Lueros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
CC -|- CATALYTIC ACTIVITY: ATP + D-ribose 5-phosphate = ADP + D-
CC ribulose 1,5-bisphosphate.
CC -|- ENZYME REGULATION: LIGHT REGULATED VIA THIOREDOXIN BY REVERSIBLE
CC OXIDATION/REDUCTION OF SULFHYDRYL/DISULFIDE GROUPS.
CC -|- PATHWAY: Calvin cycle.
CC -|- SIMILARITY: BELONGS TO THE PHOSPHORIBULOKINASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X58149; CAA41155.1; -.
DR EMBL; AC074309; AAG50797.1; -.
DR PIR; S16583; S16583.
DR SWISS-2DPAGE; P25697; ARATH.
DR InterPro; IPR001324; PRK.
DR Pfam; PF00485; PRK; 1.
DR PRINTS; PR00478; PHRIBLKINASE.
DR PROSITE; PS00567; PHOSPHORIBULOKINASE; 1.
KW Transferase; Kinase; Chloroplast; Transit peptide; Calvin cycle;
KW ATP-binding; Photosynthesis.
FT TRANSIT 1 46 CHLOROPLAST.
FT CHAIN 47 395 PHOSPHORIBULOKINASE.
FT DISULFID 61 100 BY SIMILARITY.
SQ SEQUENCE 395 AA; 44463 MW; 4660A92EF7E39BC6 CRC64;

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Query Match      33.3%; Score 61; DB 1; Length 395;
Best Local Similarity 41.4%; Pred. No. 0.29;
Matches 12; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

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QY      3 SNLSTCVLGKLSQELHKLQTYPRNTGSG 31
Db      ||||| |:::| |:::| |:::|
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Search completed: May 30, 2003, 09:50:56
Job time : 24 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 09:51:24 ; Search time 18 Seconds
(without alignments)
191.200 Million cell updates/sec

Title: SEQ1
Perfect score: 183
Sequence: 1 mcsnlstcvlgklsqelhkltprntgsgtpg 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

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2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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8:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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13:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	172	94.0	32	10	US-09-847-712-15
2	172	94.0	32	10	US-09-847-712-16
3	172	94.0	32	10	US-09-847-712-17
4	172	94.0	32	10	US-09-847-712-18
5	162	88.5	32	9	US-09-852-870A-20
6	159	86.9	32	10	US-09-847-712-10
7	158	86.3	32	9	US-09-852-870A-21
8	152	83.1	34	9	US-10-131-543-17
9	151	82.5	32	10	US-09-847-712-12
10	149	81.4	32	9	US-09-852-870A-17
11	148	80.9	35	9	US-10-131-543-26
12	147.5	80.6	34	9	US-10-131-543-25
13	147	80.3	35	9	US-10-131-543-24
14	145	79.2	32	9	US-09-852-870A-16
15	144	78.7	31	9	US-10-131-543-12
16	137	74.9	35	9	US-10-131-543-20
17	137	74.9	35	9	US-10-131-543-23
18	136.5	74.6	34	9	US-10-131-543-19
19	136.5	74.6	34	9	US-10-131-543-22

20	136.5	74.6	34	9	US-10-131-543-27
21	136	74.3	35	9	US-10-131-543-18
22	136	74.3	35	9	US-10-131-543-21
23	131	71.6	25	8	US-08-851-965-28
24	123.5	67.5	34	9	US-10-131-543-28
25	118	64.5	25	10	US-09-813-345-20
26	108	59.0	24	10	US-09-813-345-21
27	102	55.7	32	10	US-09-847-712-13
28	101	55.2	116	10	US-09-742-373-7
29	101	55.2	116	10	US-09-742-373-8
30	101	55.2	128	10	US-09-742-373-9
31	101	55.2	141	9	US-09-736-457-1822
32	101	55.2	141	9	US-09-902-941-1822
33	101	55.2	141	9	US-09-849-626-1822
34	101	55.2	141	9	US-10-017-754-1822
35	95	51.9	32	10	US-09-847-712-9
36	95	51.9	32	10	US-09-847-712-19
37	95	51.9	32	10	US-09-847-712-21
38	95	51.9	32	10	US-09-847-712-22
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40	89	48.6	32	9	US-09-852-870A-19
41	85	46.4	32	9	US-09-852-870A-18
42	74	40.4	25	10	US-09-813-345-22
43	60	32.8	11	10	US-09-746-945-3
44	56	30.6	32	10	US-09-847-712-11
45	55	30.1	664	10	US-09-815-242-13820

ALIGNMENTS

RESULT 1
US-09-847-712-15
; Sequence 15, Application US/09847712
; Patent No. US20020090646A1
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: REYNOLDS, ANGELA
; TITLE OF INVENTION: CALCITONIN-RELATED MOLECULES
; FILE REFERENCE: A-684
; CURRENT APPLICATION NUMBER: US/09/847,712
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,511
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - salmon CT
; NAME/KEY: misc.feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: An Fc domain attached at the C-terminus
US-09-847-712-15
Query Match 94.0%; Score 172; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.2e-17;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CSNLTSTCVLGKLSQELHKLTQYPRNTGSGTP 33
Db 1 CSNLTSTCVLGKLSQELHKLTQYPRNTGSGTP 32
RESULT 2
US-09-847-712-16
; Sequence 16, Application US/09847712
; Patent No. US20020090646A1
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA

```

; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: REYNOLDS, ANGELA
; TITLE OF INVENTION: CALCITONIN-RELATED MOLECULES
; FILE REFERENCE: A-684
; CURRENT APPLICATION NUMBER: US/09/847,712
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,511
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - salmon CT
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Fc domain attached at the N-terminus
US-09-847-712-16

Query Match          94.0%; Score 172; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.2e-17;
Matches 32; Conservative 0; Mismatches 0; Indels

QY      2 CSNLSCTCVLGKLSQELHKLQTYPRNTGSGTP 33
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DB       1 CSNLSCTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 3
US-09-847-712-17
; Sequence 17, Application US/09847712
; Patent No. US2002090646A1
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: REYNOLDS, ANGELA
; TITLE OF INVENTION: CALCITONIN-RELATED MOLECULES
; FILE REFERENCE: A-684
; CURRENT APPLICATION NUMBER: US/09/847,712
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,511
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - salmon CT
; NAME/KEY: misc_feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: Position 32 is linked to an identical pep
; OTHER INFORMATION: optional linker
US-09-847-712-17

Query Match          94.0%; Score 172; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.2e-17;
Matches 32; Conservative 0; Mismatches 0; Indels

QY      2 CSNLSCTCVLGKLSQELHKLQTYPRNTGSGTP 33
        |||||||
DB       1 CSNLSCTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 4
US-09-847-712-18
; Sequence 18, Application US/09847712
; Patent No. US2002090646A1
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA

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; APPLICANT: REYNOLDS, ANGELA
; TITLE OF INVENTION: CALCITONIN-RELATED MOLECULES
; FILE REFERENCE: A-684
; CURRENT APPLICATION NUMBER: US/09/847,712
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,511
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 32
; TYPE: PRT
; ORGANISM: eel
US-09-847-712-10

Query Match      86.9%; Score 159; DB 10; Length 32;
Best Local Similarity 90.6%; Pred. No. 2.le-15;
Matches 29; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY   2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
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Db   1 CSNLSTCVLGKLSQELHKLQTYPRIDVGATP 32

RESULT 7
US-09-852-870A-21
; Sequence 21, Application US/09852870A
; Patent No. US20020165132A1
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Osapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge between Cys and second Ser
US-09-852-870A-21

Query Match      86.3%; Score 158; DB 9; Length 32;
Best Local Similarity 93.8%; Pred. No. 2.9e-15;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY   2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
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Db   1 CGNLSTVGLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 8
US-10-131-543-17
; Sequence 17, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Cyv, John E.
; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131,543
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
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; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge between Cys and third Ser
US-09-852-870A-17

Query Match      81.4%; Score 149; DB 9; Length 32;
Best Local Similarity 87.5%; Pred. No. 5.2e-14;
Matches 28; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy  2 CSNLSTCVLGLKSLQELHKLQTYPRNTGSGTP 33
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Db  1 CSNLSTSVLGLKSLQELHKLQTYPRNTDVGATP 32

RESULT 11
US-10-131-543-26
; Sequence 26, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131,543
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: ACETYLTATION
; LOCATION: 1, 14
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 14
; OTHER INFORMATION: Xaa = epsilon-Lysine
; NAME/KEY: AMIDATION
; LOCATION: 17, 35
US-10-131-543-26

Query Match      80.9%; Score 148; DB 9; Length 35;
Best Local Similarity 85.7%; Pred. No. 7.9e-14;
Matches 30; Conservative 1; Mismatches 0; Indels 4; Gaps 1;

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Db  1 SNLSTCVLGLKSLCXGCELHKLQTYPRNTGSGTP 35

RESULT 12
US-10-131-543-25
; Sequence 25, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131,543
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: ACETYLTATION
; LOCATION: 1, 14
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: 17, 35
US-10-131-543-24

Query Match      80.3%; Score 147; DB 9; Length 35;
Best Local Similarity 85.7%; Pred. No. 1.1e-13;
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; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131,543
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: ACETYLTATION
; LOCATION: 1, 14
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 14
; OTHER INFORMATION: beta-Dap: 2,3 diaminopropionic acid residue
; NAME/KEY: AMIDATION
; LOCATION: 16, 34
US-10-131-543-25

Query Match      80.6%; Score 147.5; DB 9; Length 34;
Best Local Similarity 88.2%; Pred. No. 9e-14;
Matches 30; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

Qy  3 SNLSTCVLGLKLS---QELHKLQTYPRNTGSGTP 33
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  1 SNLSTCVLGLKSLCKCKELHKLQTYPRNTGSGTP 34

RESULT 13
US-10-131-543-24
; Sequence 24, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131,543
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: ACETYLTATION
; LOCATION: 1, 14
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: 17, 35
US-10-131-543-24

Query Match      80.3%; Score 147; DB 9; Length 35;
Best Local Similarity 85.7%; Pred. No. 1.1e-13;
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Matches 30; Conservative 1; Mismatches 0; Indels 4; Gaps 1;
 QY 3 SNLSTCVLGKLS---QELHKLQTYPRNTGSGTP 33
 ||||| ||||| : ||||| ||||| ||||| |||||
 Db 1 SNLSTCVLGKLSGGGCKELHKLQTYPRNTGSGTP 35

RESULT 14
 US-09-852-870A-16
 ; Sequence 16, Application US/09852870A
 ; Patent No. US20020165132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodman, Murray
 ; APPLICANT: Osapay, George
 ; TITLE OF INVENTION: Lanthionin Bridged Proteins
 ; FILE REFERENCE: LKR 9122-D
 ; CURRENT APPLICATION NUMBER: US/09/852,870A
 ; CURRENT FILING DATE: 2001-05-10
 ; PRIOR APPLICATION NUMBER: US 09/384,601
 ; PRIOR FILING DATE: 1999-08-26
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 16
 ; LENGTH: 32
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Cys-Ser Lanthionine bridge between Cys and second Ser
 US-09-852-870A-16

Query Match 79.2%; Score 145; DB 9; Length 32;
 Best Local Similarity 84.4%; Pred. No. 1.9e-13;
 Matches 27; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
 . | |||| | |||| | |||| | |||| | |||| | ||||
 Db 1 CGNLSTVGLGKLSQELHKLQTYPRNTDVGATP 32

RESULT 15
 US-10-131-543-12
 ; Sequence 12, Application US/10131543
 ; Publication No. US20030072709A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pearson, Daniel A.
 ; APPLICANT: Cyr, John E.
 ; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
 ; FILE REFERENCE: 09744-016001
 ; CURRENT APPLICATION NUMBER: US/10/131,543
 ; CURRENT FILING DATE: 2002-04-24
 ; PRIOR APPLICATION NUMBER: US 09/694,992
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: PCT/US01/50423
 ; PRIOR FILING DATE: 2001-10-24
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic construct
 ; FEATURE:
 ; NAME/KEY: ACETYLATION
 ; LOCATION: 1
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: 6
 ; OTHER INFORMATION: Xaa = Hhc: Homohomocysteine
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: 13

; OTHER INFORMATION: BAT: N6,N9-bis (mercapto-2-methylpropyl)-6,9-diazanonoic aci
 ; FEATURE:
 ; NAME/KEY: AMIDATION
 ; LOCATION: 31
 US-10-131-543-12

Query Match 78.7%; Score 144; DB 9; Length 31;
 Best Local Similarity 93.5%; Pred. No. 2.5e-13;
 Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 SNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 SNLSTXVLGKLSQELHKLQTYPRNTGSGTP 31

Search completed: May 30, 2003, 09:56:42
 Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 09:49:41 ; Search time 35 seconds
(without alignments)
129,443 Million cell updates/sec

Title: SEQ1
Perfect score: 183
Sequence: 1 mcsnlstcvlgklsqelghklqtpyrtngstpg 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*

- 1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SID2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SID2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SID2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SID2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SID2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SID2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SID2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SID2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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- 18: /SID2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	183	100.0	34	7 AAP60792	Fish calcitonin de
2	183	100.0	34	9 AAP80414	Salmon calcitonin
3	183	100.0	34	9 AAP80676	Salmon calcitonin-
4	183	100.0	34	9 AAP81041	Sequence of salmon
5	183	100.0	53	22 AAB61575	Partial protein se
6	178	97.3	33	20 ABB08914	Synthetic CT pepti
7	178	97.3	136	23 ABBG0636	Salmon calcitonin.
8	177	96.7	33	13 AAR30341	[Met 0]-salmon cal
9	174	95.1	33	13 AAR30338	[Leu 0]-salmon cal
10	174	95.1	33	13 AAR30314	[Met 0, Leu 8]-sal

11	173	94.5	33	13 AAR30339	[Val 0]-salmon cal
12	173	94.5	33	13 AAR30340	[Ile 0]-salmon cal
13	172	94.0	32	3 AAP20308	Peptide prep. by
14	172	94.0	32	5 AAP40289	Sequence of D-Arg
15	172	94.0	32	8 AAP71360	1,7-di-S-acetamido
16	172	94.0	32	8 AAP71487	sequence of N(alph
17	172	94.0	32	14 AAR36987	Anylin antagonist
18	172	94.0	32	15 AAR47664	Salmon calcitonin.
19	172	94.0	32	15 AAR59790	Fragment 6 of Salm
20	172	94.0	32	15 AAR59791	Fragment 7 of Salm
21	172	94.0	32	15 AAR60152	Salmon calcitonin
22	172	94.0	32	16 AAR66858	Calcitonin deriv.
23	172	94.0	32	16 AAR84250	Calcitonin peptide
24	172	94.0	32	17 AAR10575	Salmon calcitonin
25	172	94.0	32	18 AAR22542	Anylin agonist pep
26	172	94.0	32	20 AAY04000	Salmon calcitonin,
27	172	94.0	32	20 AAY93528	Salmon calcitonin,
28	172	94.0	32	21 AAY95663	Salmon calcitonin.
29	172	94.0	32	22 AAB91046	Calcitonins (CT) a
30	172	94.0	32	22 AAE14323	Salmon calcitonin
31	172	94.0	32	23 AAE14324	Salmon calcitonin
32	172	94.0	32	23 AAR30342	[Thr 0]-salmon cal
33	172	94.0	33	13 AAR30343	[Ser 0]-salmon cal
34	172	94.0	33	13 AAR30344	[Ala 0]-salmon cal
35	172	94.0	33	13 AAR30345	[Nva 0]-salmon cal
36	172	94.0	33	13 AAR30346	[Nle 0]-salmon cal
37	172	94.0	35	13 AAR20042	Calcitonin analogue
38	172	94.0	64	23 AAE14325	Salmon calcitonin
39	172	94.0	64	23 AAE14326	Salmon calcitonin
40	172	94.0	271	23 AAE14335	Fc-calcitonin fusi
41	172	94.0	33	13 AAR30311	[Leu 0,8]-salmon c
42	171	93.4	33	13 AAR30312	[Val 0, Leu 8]-sal
43	170	92.9	33	13 AAR30313	[Ile 0, Leu 8]-sal
44	170	92.9	33	13 AAR30313	Salmon 8-Methionin
45	169	92.3	32	7 AAP60858	

ALIGNMENTS

RESULT 1	
AAP60792	standard; Protein; 34 AA.
XX	AAP60792:
XX	
XX	17-JUL-1991 (first entry)
XX	
XX	Fish calcitonin derivative.
DE	
XX	
XX	pSCTL; E.coli RRI.
KW	
XX	Synthetic.
OS	
XX	
PH	Key
FT	Protein
FT	2..34
FT	/label= Reptide of claim 8
FT	Misc-difference 27
FT	/label= May be Asn or Asp
FT	Misc-difference 28
FT	/label= May be Thr or Val
FT	Misc-difference 30
FT	/label= May be Ser or Ala
XX	
XX	WO8601226-A.
PN	
XX	27-FEB-1986.
PD	
XX	
XX	16-AUG-1985; 85WO-JP00459.
PF	
XX	
XX	18-JUN-1985; 85JP-0130815.
PR	
PR	17-AUG-1984; 84JP-0170492.
PR	11-MAY-1985; 85JP-0098891.

PR 28-MAY-1985; 85JP-0113254.
 XX (SAGA) SAGAMI CHEM RES CENTRE.
 PA (CENG) CENTRAL GLASS KK.
 PA (HODO) HODOGAYA CHEMICAL KK.
 PA (NIPS) NIPPON SODA KK.
 PA (NISC) NISSAN CHEMICAL INDS LTD.
 PA (TOVJ) TOYO SODA MFG KK.
 XX Omori M, Miki T, Narushima H, Ikari T, Saito A, Ikushima N;
 PI Matsumoto R, Watanabe K;
 XX WPI; 1986-068975/10.
 DR N-PSDB; AAN60710.
 XX Biologically active fish calcitonin contg. extra glycine at
 PT C-terminal - convertible to natural form and prepd. using E.coli
 PT recombinant transform.
 XX Disclosure; Fig 1; 106pp; Japanese.
 XX The sequence encodes a fish calcitonin derivative which may be used
 CC for the construction of expression vector pSCT1 capable of
 CC transforming an E.coli host for the efficient large scale expression
 CC of the product.
 XX Sequence 34 AA;
 SQ
 Query Match 100.0%; Score 183; DB 7; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MCSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34
 DB 1 MCSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34
 RESULT 2
 AAP80414
 ID AAP80414 standard; protein; 34 AA.
 XX
 AC AAP80414;
 XX
 DT 29-OCT-1990 (first entry)
 XX
 DE Salmon calcitonin produced by recombinant methods.
 XX
 KW Calcitonin; beta-galactosidase; interferon; proinsulin; secretin; inter-
 KW leukin-2; hirudin; growth hormone releasing factor.
 XX
 OS synthetic.
 XX
 PN EP286956-A.
 XX
 PD 19-OCT-1988.
 XX
 PF 06-APR-1988; 88EP-0105438.
 XX
 PR 19-FEB-1988; 88DE-3805150.
 XX
 PR 19-FEB-1988; 88DE-3712361.
 XX
 PA (FARH) HOECHST AG.
 XX
 PI Wetekam W, Jansen HW, Becker W;
 XX
 DR WPI; 1988-294356/42.
 DR N-PSOB; AAN80970.
 XX
 PT Recombinant polypeptide prodn. - via fusion protein with modified beta-
 PT galactosidase
 XX
 PS Example; Page 11; 20pp; German.
 XX

CC This salmon calcitonin protein is produced as a fusion protein. The
 CC process can also be used to produce e.g. interferon and proinsulin.
 XX Sequence 34 AA;
 Query Match 100.0%; Score 183; DB 9; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MCSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34
 DB 1 MCSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34
 RESULT 3
 AAP80676
 ID AAP80676 standard; protein; 34 AA.
 XX
 AC AAP80676;
 XX
 DT 24-OCT-1990 (first entry)
 XX
 DE Salmon calcitonin-Gly 33.
 XX
 KW 3' terminal hairpin loop; double stranded DNA synthesis;
 KW salmon calcitonin-Gly 33.
 XX
 OS synthetic.
 XX
 PN EP292802-A.
 XX
 PD 30-NOV-1988.
 XX
 PF 13-MAY-1988; 88EP-0107660.
 XX
 PR 23-MAY-1987; 87DE-2717436.
 XX
 PA (FARH) HOECHST AG.
 XX
 PI Uhlmann E, Hein F;
 XX
 DR WPI; 1988-339391/48.
 DR N-PSDB; N81269
 XX
 PT Double stranded DNA prodn -
 PT from single strand with terminal hairpin loop by filling in
 PT second strand, then opening or removing hair pin
 XX
 PS Disclosure; ; pp; German.
 XX
 CC DNA(ds) encoding salmon calcitonin was synthesised as a single
 CC coding strand with a terminal hairpin primer. The complementary
 CC strand was synthesised from the primer.
 CC Use of oligonucleotides with a hairpin loop primer avoids the need
 CC for chemically synthesising both strands. Also the filling in step
 CC can be performed using labelled nucleotides to give products
 CC suitable for use as probes. Mutagenic primers can be used to
 CC introduce site specific mutations.
 CC See also AAN81267 and AAN81268.
 XX
 SQ Sequence 34 AA;
 Query Match 100.0%; Score 183; DB 9; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MCSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34
 DB 1 MCSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34
 RESULT 4
 AAP81041

Seq1: 03-DEC-1990 (first entry)

Sequence of salmon calcitonin I having an additional C-terminal glycine.

Hypocalcaemic; hypophosphataemia peptide hormone; pancreatitis therapy.

Salmon.

EP261552-A.

30-MAR-1988.

15-SEP-1987; 87EP-0113445.

20-SEP-1986; 86DE-3632037.

(FARR) HOECHST AG.

Hein F, Jansen HW, Muller H, Uhlmann E;

WPI; 1988-085860/13.

N-PSDB; AAN81385.

Salmon calcitonin I derivs. prepn.

by inserting new plasmid encoding for the deriv. into e.g.

Escherichia coli gene

Disclosure; ; p; German.

Calcitonin is a hypocalcaemic and hypophosphataemia peptide hormone which regulates serum levels of Ca. It is useful for treating Ca metabolic disorders, as an analgesic and for treating acute pancreatitis inhibiting enzyme secretion.

Seq1: 03-DEC-1990 (first entry)

Sequence 34 AA;

Query Match 100.0%; Score 183; DB 9; Length 34;

Best Local Similarity 100.0%; Pred. No. 5.4e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSNLSTCVLGKLSOELHKLQTYPTNTGSGTGP 34

Db 1 MCSNLSTCVLGKLSOELHKLQTYPTNTGSGTGP 34

RESULT 5

ID AAB61575 standard; Protein; 53 AA.

XX AAB61575;

AC 03-APR-2001 (first entry)

Partial protein sequence of pCLYSM.

Transgenic; milk; lysozyme; pCLYSM; salmon; calcitonin.

Unidentified.

XX WO200100855-A1.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-GB02459.

XX 23-JUN-1999; 99GB-0014733.

XX 10-AUG-1999; 99US-0147819.

XX (PPLT-) PPL THERAPEUTICS SCOTLAND LTD.

XX Cottingham IR, McCreath GE;

XX WPI; 2001-137958/14.

XX N-PSDB; AAF28653.

Producing peptides for use as medicaments, nutritional additives or research tools, comprising expressing a fusion protein, which contains the peptide linked to a lysozyme fusion partner protein, in the milk of a transgenic mammal

Example 1; Fig 1; 57pp; English.

The present invention relates to a method for producing a peptide. The method comprises expressing in the milk of a transgenic non-human placental mammal a fusion protein, comprising the peptide to be expressed linked to lysozyme (a fusion partner protein). The method is useful for producing proteins or peptides that are useful as medicaments, nutritional additives or research tools. The present sequence is a partial DNA sequence of pCLYSM. pCLYSM was designed to express a human lysozyme-salmon calcitonin fusion protein in the milk of transgenic animals. The fusion protein allows the release of calcitonin from the end of a linker arm fused to the lysozyme C terminal by cyanogen bromide chemical cleavage. pCLYSM consists of the ovine beta-lactoglobulin (BLG) promoter and 5' UTR, human lysozyme gene, peptide linker (see AAB61572), CNBr cleavage site and salmon calcitonin coding sequence, ovine BLG 3' UTR, polyadenylation site and flanking region, chick alpha-globin insulator region and the pUC18 bacterial plasmid vector. The present sequence is a partial protein sequence of pCLYSM comprising the peptide linker, the CNBr cleavage site and the calcitonin peptide sequence.

Seq1: 03-DEC-1990 (first entry)

Query Match 100.0%; Score 183; DB 22; Length 53;

Best Local Similarity 100.0%; Pred. No. 8.7e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSNLSTCVLGKLSOELHKLQTYPTNTGSGTGP 34

Db 20 MCSNLSTCVLGKLSOELHKLQTYPTNTGSGTGP 53

RESULT 6

ID ABB08914 standard; peptide; 33 AA.

XX ABB08914;

XX 16-JUL-2002 (first entry)

Synthetic CT peptide sCT(Gly).

TNF; tumour necrosis factor; beta-sheet; fusion protein; recombinant production; Escherichia coli; TNF fusion vector;

PT7-T150; pT7-T57; CT; sCT; pT150-sCT(Gly).

XX Synthetic.

XX KRL33475-B1.

XX 21-APR-1998.

XX 04-APR-1994; 94KR-0007018.

XX 04-APR-1994; 94KR-0007018.

XX (HANI-) HANIL SYNTHETIC FIBER CO LTD.

XX Shin H, Jang S, Kim D, Kang S;

XX WPI; 1999-617508/53.

CC analogues can be used to
 CC is or to influence bone
 CC treating e.g. Vitamin D
 CC idiopathic hypercalcaemia of
 CC reduction of bone pain
 CC Intoxication, hyperparathyroidism, idiopathic hypercalcaemia of
 CC peptides also inhibit gastrin secretion making them useful to
 CC treat acute pancreatitis and gastrointestinal disorders, esp.
 CC gastric ulcers.

XX SQ Sequence 33 AA;
 Query Match 96.7%; Score 177; DB 13; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3.2e-16;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSNLSTCVLGLKLSQELHKLQTYPRNTGSGTP 33
 :|||||
 Db 1 MCSNLSTCVLGLKLSQELHKLQTYPRNTGSGTP 33

RESULT 9
 AAR30338
 ID AAR30338 standard; peptide; 33 AA.
 AC AAR30338;
 DT 30-APR-1993 (first entry)
 DE [Leu 0]-salmon calcitonin.
 DE sCT; calcium regulation; thyroid gland; hormone; bone resorption.
 KW Salmon.
 XX Key Location/Qualifiers
 FT Misc-difference 1 /note= "designated position 0, i.e. additional
 FT Disulfide-bond 2..8 N-terminal amino acid"
 FT Modified-site 33 /note= "amidated"

XX WO9221369-A.
 XX 10-DEC-1992.
 XX 03-JUN-1992; 92WO-US04854.
 XX 05-JUN-1991; 91US-0711180.
 XX (VICA-) VICAL INC.
 XX Basava C, Hostetler KY;
 XX WPI: 1992-433374/52.
 XX New synthetic calcitonin peptide(s) are hypocalcaemic agents -
 XX for treating Paget's disease, osteoporosis, bone fracture, etc.
 XX with lower immunogenicity than natural calcitonin(s)

XX Claim 3; Page 28; 42pp: English.
 XX This hypocalcaemic peptide is a specifically claimed example of
 XX calcitonin analogues which have amino acid additions at the
 XX N-terminal which, alone or with other substitutions, and with
 XX deletions at other residues, act to improve potency, prolong
 XX duration of the hormonal effect and increase oral or nasal
 XX bioavailability, c.f. native CTS. The analogues can be used to
 XX reduce or normalise serum calcium levels or to influence bone
 XX metabolism. They are thus useful for treating e.g. Vitamin D
 XX intoxication, hyperparathyroidism, idiopathic hypercalcaemia of
 XX infancy, bone fracture, rickets, osteoporosis and bone pain.

CC associated with these diseases or with articular rheumatism. The
 CC peptides also inhibit gastrin secretion making them useful to
 CC treat acute pancreatitis and gastrointestinal disorders, esp.
 CC gastric ulcers.

XX SQ Sequence 33 AA;
 Query Match 95.1%; Score 174; DB 13; Length 33;
 Best Local Similarity 97.0%; Pred. No. 8e-16;
 Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSNLSTCVLGLKLSQELHKLQTYPRNTGSGTP 33
 :|||||
 Db 1 LCSNLSTCVLGLKLSQELHKLQTYPRNTGSGTP 33

RESULT 10
 AAR30314
 ID AAR30314 standard; peptide; 33 AA.
 AC AAR30314;
 DT 30-APR-1993 (first entry)
 DE [Met 0, Leu 8]-salmon calcitonin.
 DE sCT; calcium regulation; thyroid gland; hormone; bone resorption.
 KW Salmon.
 XX Key Location/Qualifiers
 FT Misc-difference 1 /note= "designated position 0, i.e. additional
 FT Disulfide-bond 2..8 N-terminal amino acid"
 FT Misc-difference 9 /note= "designated position 8 in sCT,
 FT Modified-site 33 Leu replaces Val"
 FT WO9221369-A.
 XX 10-DEC-1992.
 XX 03-JUN-1992; 92WO-US04854.
 XX 05-JUN-1991; 91US-0711180.
 XX (VICA-) VICAL INC.
 XX Basava C, Hostetler KY;
 XX WPI: 1992-433374/52.

XX New synthetic calcitonin peptide(s) are hypocalcaemic agents -
 XX for treating Paget's disease, osteoporosis, bone fracture, etc.
 XX with lower immunogenicity than natural calcitonin(s)
 XX Example 16c; Page 28; 42pp: English.
 XX This hypocalcaemic peptide is an example of novel
 XX calcitonin analogues which have amino acid additions at the
 XX N-terminal which, alone or with other substitutions, and with
 XX deletions at other residues, act to improve potency, prolong
 XX duration of the hormonal effect and increase oral or nasal
 XX bioavailability, c.f. native CTS. The analogues can be used to
 XX reduce or normalise serum calcium levels or to influence bone
 XX metabolism. They are thus useful for treating e.g. Vitamin D
 XX intoxication, hyperparathyroidism, idiopathic hypercalcaemia of
 XX infancy, bone fracture, rickets, osteoporosis and bone pain
 XX associated with these diseases or with articular rheumatism. The
 XX peptides also inhibit gastrin secretion making them useful to

Orlowski PC Savler JK Colescott PL Stahl GL Enkoi T Geever JE.

Fri May 30 10:10:21 2003

seq1.rag

Page 8

PI Planigan E;
XX
DR WPI: 1987-129186/18.
XX
PT New salmon and eel calcitonin analogues - do not have disulphide
XX bond connecting cysteine residues.
PS
PS Claim 1: page 9-10; 10pp; English.
XX
CC The salmon calcitonin analogue has the biological activity of the same
CC type of calcitonin and comparable potency to known calcitonins.
CC It differs in not having a disulphide bond connecting the cysteines at
CC positions 1 and 7. In a test, 3 and 9 µg/100 g body weight of the
CC standard salmon calcitonin and 0.2 ml/100 g body weight of the
CC analogue were given to different rats. Serum calcium was determined
CC after 1 hr. The standard salmon calcitonin was found to contain
CC 4000 IU/mg, whereas the analogue assayed at 4250 IU/mg.
XX
SQ Sequence 32 AA:
Query Match 94.0%; Score 172; DB 8; Length 32;
Best Local Similarity 100.0%; Posed No
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 CSNLSVCVLGKLSQELKLOTYPRTNTGSGTP 33
DB 1 CSNLSVCVLGKLSQELKLOTYPRTNTGSGTP 32

Search completed: May 30, 2003, 09:50:26
Job time : 37 secs

A;Gene: CT

C, Superfamily: calcitonin

Query Match 97.3%; Score 178; DB 1; Length 59;
 Best Local Similarity 100.0%; Pred. No. 8.8e-18;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSVCVLGKLSOELHKLQTYPRNTGSGTPG 34
 |||||
 Db 6 CSNLSVCVLGKLSOELHKLQTYPRNTGSGTPG 38

RESULT 3

TCO2C

calcitonin 1 precursor - salmon
 C:Species: Oncorhynchus sp. (salmon)
 C:Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
 C:Accession: A31229; A93772; A01530
 R:Poesschl, E.; Lindley, I.; Hofer, E.; Seifert, J.M.; Brunowsky, W.; Besemer, J.
 FEBS Lett. 226, 96-100, 1987
 A:Title: The structure of procalcitonin of the salmon as deduced from its cDNA sequence.
 A:Reference number: A31229; MUID:88083644; PMID:3691820
 A:Accession: A31229
 A:Molecule type: mRNA
 A:Residues: 1-136 <PRO>
 A:Cross-references: GB:Y00765; NID:G64312; PIDN:CAA68734.1; PID:G64313
 A:Note: The species of the source is not indicated but is designated as Oncorhynchus ket
 R:Niall, H.D.; Keutmann, H.T.; Copp, D.H.; Potts Jr., J.T.
 Proc. Natl. Acad. Sci. U.S.A. 64, 771-778, 1969
 A:Title: Amino acid sequence of salmon ultimobranchial calcitonin.
 A:Reference number: A93772; MUID:70053602; PMID:5361048
 A:Accession: A93772
 A:Molecule type: protein
 A:Residues: 83-114 <NTA>
 R:Guttmann, S.; Pless, J.; Huguenin, R.L.; Sandrin, E.; Bossert, H.; Zehnder, K.
 Helv. Chim. Acta 52, 1789-1795, 1969
 A:Title: Synthese von Salm-calcitonin, einem hochaktiven hypocalcaemischen Hormon.
 A:Reference number: A91631; MUID:70067983; PMID:5361511
 A:Contents: annotation; synthesis of hormone
 A:Note: the proposed structure of the natural hormone was supported by that of the synth
 C:Superfamily: calcitonin
 C:Keywords: amidated carboxyl end; hormone
 F:1-25/Domains: signal sequence #status predicted <SIG>
 F:26-136/Product: procalcitonin 1 #status predicted <PCA>
 F:83-114/Product: calcitonin 1 #status experimental <CAI>
 F:83-89/Disulfide bonds: #status experimental
 F:114/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl

Query Match 97.3%; Score 178; DB 1; Length 136;
 Best Local Similarity 100.0%; Pred. No. 2e-17;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSVCVLGKLSOELHKLQTYPRNTGSGTPG 34
 |||||
 Db 83 CSNLSVCVLGKLSOELHKLQTYPRNTGSGTPG 115

RESULT 4

TCO2C

calcitonin - Japanese eel
 C:Species: Anguilla japonica (Japanese eel)
 C:Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 08-Dec-1995
 C:Accession: A01529
 R:Noda, T.; Narita, K.
 J. Biochem. 79, 353-359, 1976
 A:Title: Amino acid sequence of eel calcitonin.
 A:Reference number: A01529
 A:Accession: A01529
 A:Molecule type: protein
 A:Residues: 1-32 <NOO>
 C:Superfamily: calcitonin
 C:Keywords: amidated carboxyl end
 F:1-7/Disulfide bonds: #status experimental
 F:32/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 86.9%; Score 159; DB 1; Length 32;
 Best Local Similarity 90.6%; Pred. No. 2.2e-15;
 Matches 29; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 CSNLSVCVLGKLSOELHKLQTYPRNTGSGTPG 33
 |||||
 Db 1 CSNLSVCVLGKLSOELHKLQTYPRNTGSGTPG 32

RESULT 5

TCO2C

calcitonin 2 - sockeye salmon
 C:Species: Oncorhynchus nerka (sockeye salmon)
 C:Date: 22-May-1981 #sequence_revision 22-May-1981 #text_change 23-Aug-1996
 C:Accession: A01531
 R:Keutmann, H.T.; Lequin, R.M.; Habener, J.F.; Singer, F.R.; Niall, H.D.; Potts Jr.,
 In Endocrinology 1971: Proceedings of the Third International Symposium, Taylor, S.,
 A:Title: Chemistry and physiology of the calcitonins: some recent advances.
 A:Reference number: A04616
 A:Accession: A01531
 A:Molecule type: protein
 A:Residues: 1-32 <KEU>
 R:Pless, J.; Bauer, W.; Bossert, H.; Zehnder, K.; Guttmann, S.
 Nature New Biol. 240, 62-63, 1972
 A:Title: Synthesis of two natural salmon calcitonins.
 A:Reference number: A93406; MUID:73047885; PMID:4508400
 A:Contents: annotation; synthesis
 A:Note: the synthetic hormones were the same as the natural ones on the basis of phys
 an calcitonins 1 or 2
 C:Superfamily: calcitonin
 C:Keywords: amidated carboxyl end; hormone
 F:1-7/Disulfide bonds: #status experimental
 F:32/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 85.8%; Score 157; DB 1; Length 32;
 Best Local Similarity 87.5%; Pred. No. 4.1e-15;
 Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 CSNLSVCVLGKLSOELHKLQTYPRNTGSGTPG 33
 |||||
 Db 1 CSNLSVCVLGKLSOELHKLQTYPRNTGSGTPG 32

RESULT 6

TCO2C

calcitonin 2 - chum salmon
 C:Species: Oncorhynchus keta (chum salmon)
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 23-Aug-1996
 C:Accession: C01531; A01531
 R:Keutmann, H.T.; Lequin, R.M.; Habener, J.F.; Singer, F.R.; Niall, H.D.; Potts Jr.,
 In Endocrinology 1971: Proceedings of the Third International Symposium, Taylor, S.,
 A:Title: Chemistry and physiology of the calcitonins: some recent advances.
 A:Reference number: A04616
 A:Accession: C01531
 A:Molecule type: protein
 A:Residues: 1-32 <KEU>
 R:Pless, J.; Bauer, W.; Bossert, H.; Zehnder, K.; Guttmann, S.
 Nature New Biol. 240, 62-63, 1972
 A:Title: Synthesis of two natural salmon calcitonins.
 A:Reference number: A93406; MUID:73047885; PMID:4508400
 A:Contents: annotation; synthesis
 A:Note: the synthetic hormones were the same as the natural ones on the basis of phys

Query Match 85.8%; Score 157; DB 1; Length 32;
 Best Local Similarity 87.5%; Pred. No. 4.1e-15;
 Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 CSNLSVCVLGKLSOELHKLQTYPRNTGSGTPG 33
 |||||
 Db 1 CSNLSVCVLGKLSOELHKLQTYPRNTGSGTPG 32

```

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
    |||||
Db 1 CSNLSTCVLGKLSQDLHLKLQTFPRNTGAGVP 32

RESULT 7
TCOIN2P
C:Species: Oncorhynchus gorbuscha (pink salmon)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 23-Aug-1996
R:Keutmann, H.T.; Leguin, R.M.; Habener, J.F.; Singer, F.R.; Niall, H.D.; Potts Jr., J.T.
in Endocrinology 1971: Proceedings of the Third International Symposium, Taylor, S., ed.
A:Title: Chemistry and physiology of the calcitonins: some recent advances.
A:Reference number: A04616
A:Accession: B01531
A:Molecule type: protein
R:Residues: 1-32 <KEU>
R:Pless, J.; Bauer, W.; Bossert, H.; Zehnder, K.; Guttman, S.
Nature New Biol. 240, 62-63, 1972
A:Title: Synthesis of two natural salmon calcitonins.
A:Reference number: A93406; MUID:73047885; PMID:4508400
A:Contents: annotation; synthesis
A>Note: the synthetic hormones were the same as the natural ones on the basis of physica
an calcitonins 1 or 2
C:Superfamily: calcitonin
C:Keywords: amidated carboxyl end; hormone
F:1-7/Disulfide bonds: #status experimental
F:32/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 85.8%; Score 157; DB 1; Length 32;
Best Local Similarity 87.5%; Pred. No. 4.1e-15;
Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
    |||||
Db 1 CSNLSTCVLGKLSQDLHLKLQTFPRNTGAGVP 32

RESULT 8
TCCH
C:Species: Gallus gallus (chicken)
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 18-Jun-1999
C:Accession: S00153; A25725; A24415; I50182; A22467
R:Minvielle, S.; Cressent, M.; Delehay, M.C.; Segond, N.; Milhaud, G.; Jullienne, A.; M
FEBS Lett. 223, 63-68, 1987
A:Title: Sequence and expression of the chicken calcitonin gene.
A:Reference number: S00153; MUID:88030046; PMID:3666142
A:Accession: S00153
A:Molecule type: DNA
A:Residues: 1-138 <MIN>
A:Cross-references: EMBL:X06311
A>Note: the sequences of codons 31-33 and 34-38 are interchanged in this reference; the
R:Lasmoles, F.; Jullienne, A.; Day, F.; Minvielle, S.; Milhaud, G.; Moukhtar, M.S.
EMBO J. 4, 2603-2607, 1985
A:Title: Elucidation of the nucleotide sequence of chicken calcitonin mRNA: direct evide
A:Reference number: A25725; MUID:86030240; PMID:4054101
A:Accession: A25725
A:Molecule type: mRNA
A:Residues: 12-55, 'E', 57-138 <LAS>
A:Cross-references: EMBL:X03012; MUID:963157; PIDN:CAA26796.1; PID:963158
R:Honna, T.; Watanabe, M.; Hirose, S.; Kanai, A.; Kangawa, K.; Matsuo, H.
J. Biochem. 100, 459-467, 1986
A:Title: Isolation and determination of the amino acid sequence of chicken calcitonin I
A:Reference number: A24415; MUID:87057104; PMID:3782060
A:Accession: A24415
A:Molecule type: protein
A:Residues: 1-32 <HOM>
R:Lasmoles, F.; Jullienne, A.; Desplan, C.; Milhaud, G.; Moukhtar, M.S.
FEBS Lett. 180, 113-116, 1985
A:Title: Structure of chicken calcitonin predicted by partial nucleotide sequence of its

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A:Reference number: I50182; MUID:85102042; PMID:3838160
A:Accession: I50182
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 71-117 <LA2>
A:Cross-references: GB:M27563; NID:g211373; PIDN:AAA48648.1; PID:g211374
C:Comment: The calcitonin gene codes for two mRNA species by tissue-specific alternat
ripheral nervous system codes for calcitonin gene-related peptide.
C:Genetics:
A:Introns: 29/2; 73/2
C:Superfamily: calcitonin
C:Keywords: alternative splicing; amidated carboxyl end; hormone
F:82-113/Product: calcitonin #status experimental <MAT>
F:82-86/Disulfide bonds: #status experimental
F:113/Modified site: amidated carboxyl end (Pro) (amide in mature form from following
Query Match 85.8%; Score 157; DB 1; Length 138;
Best Local Similarity 84.8%; Pred. No. 1.7e-14;
Matches 28; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTPG 34
    |||||
Db 82 CASLSTCVLGKLSQELHKLQTYPRTDVGATPG 114

RESULT 9
TCOIN3
C:Species: Oncorhynchus kisutch (coho salmon)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 08-Dec-1995
C:Accession: B01531; A01531
R:Keutmann, H.T.; Leguin, R.M.; Habener, J.F.; Singer, F.R.; Niall, H.D.; Potts Jr.,
in Endocrinology 1971: Proceedings of the Third International Symposium, Taylor, S.,
A:Title: Chemistry and physiology of the calcitonins: some recent advances.
A:Reference number: A04616
A:Accession: B01531
A:Molecule type: protein
R:Pless, J.; Bauer, W.; Bossert, H.; Zehnder, K.; Guttman, S.
Nature New Biol. 240, 62-63, 1972
A:Title: Synthesis of two natural salmon calcitonins.
A:Reference number: A93406; MUID:73047885; PMID:4508400
A:Contents: annotation; synthesis
A>Note: the synthetic hormones were the same as the natural ones on the basis of phys
an calcitonins 1 or 2
C:Superfamily: calcitonin
C:Keywords: amidated carboxyl end
F:1-7/Disulfide bonds: #status experimental
F:32/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 84.2%; Score 154; DB 1; Length 32;
Best Local Similarity 84.4%; Pred. No. 1.1e-14;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
    |||||
Db 1 CSNLSTCVLGKLSQDLHLKLQTFPRNTGAGVP 32

RESULT 10
TCRT
C:Contains: amino-terminal procalcitonin cleavage peptide (N-proCT); carboxyl-termina
C:Species: Rattus norvegicus (Norway rat)
C>Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 18-Jun-1999
C:Accession: A94259; A93855; A91236; I52379; A01525
R:Jacobs, J.W.; Goodman, R.H.; Chin, W.W.; Bee, P.C.; Habener, J.F.; Bell, N.H.; Pott
Science 213, 457-459, 1981
A:Title: Calcitonin messenger RNA encodes multiple polypeptides in a single precursor
A:Reference number: A94259; MUID:81225842; PMID:6264603
A:Accession: A94259
A:Molecule type: mRNA
A:Residues: 1-136 <JAC>

```


Query Match 49.2%; Score 90; DB 2; Length 67;
 Best Local Similarity 51.5%; Pred. No. 1.9e-05;
 Matches 17; Conservative 5; Mismatches 11; Indels 0;
 Gaps 0;
 F53/Modified site: amidated carboxyl end (Pro) (amide in mature form from following

Search completed: May 30, 2003, 09:51:17
Job time : 16 secs

GenCore version 5.1.1.6
 Copyright (c) 1993 - 2003 CompuGen Ltd.
 OM protein - protein search, using sw model
 Run on: May 30, 2003, 09:49:44 ; Search time 79 Seconds
 (without alignments)
 88,679 Million cell updates/sec

Title: SEQ1
 Perfect score: 183
 Sequence: 1 mesnlstevlgklsqelkhkltprntngstgtpg 34
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 671580 seqs, 206047115 residues
 Total number of hits satisfying chosen parameters: 671580
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Result No.	Score	Query Match	Length	ID	Description
1	178	97.3	56	Q91157	Q91157 oncorhynch
2	178	97.3	59	Q91970	Q91970 oncorhynch
3	178	97.3	62	Q92163	Q92163 oncorhynch
4	172	94.0	32	Q8Q84	Q8Q84 oncorhynch
5	172	94.0	32	Q8Q82	Q8Q82 oncorhynch
6	172	94.0	32	Q8Q83	Q8Q83 oncorhynch
7	172	94.0	32	Q8Q72	Q8Q72 salmo salar
8	172	94.0	32	Q8Q71	Q8Q71 oncorhynch
9	172	94.0	32	Q8Q70	Q8Q70 salvelinus
10	169	92.3	32	Q8Q68	Q8Q68 oncorhynch
11	166	90.7	136	Q8Q78	Q8Q78 fugu rubrip
12	159	86.9	32	Q8PS21	Q8PS21 carassius a
13	158	86.3	62	Q79813	Q79813 oncorhynch
14	157	85.8	65	Q9W623	Q9W623 gallus gall
15	156	85.2	50	Q9QYCA	Q9QYCA paralichthy
16	112	61.2	140	Q9NOV5	Q9NOV5 equus caball

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result ID	Score	Query Match	Length	ID	Description
Q91157	178	97.3	56	Q91157	Q91157 oncorhynch
Q91157	178	97.3	59	Q91970	Q91970 oncorhynch
Q91157	178	97.3	62	Q92163	Q92163 oncorhynch
Q91157	172	94.0	32	Q8Q84	Q8Q84 oncorhynch
Q91157	172	94.0	32	Q8Q82	Q8Q82 oncorhynch
Q91157	172	94.0	32	Q8Q83	Q8Q83 oncorhynch
Q91157	172	94.0	32	Q8Q72	Q8Q72 salmo salar
Q91157	172	94.0	32	Q8Q71	Q8Q71 oncorhynch
Q91157	172	94.0	32	Q8Q70	Q8Q70 salvelinus
Q91157	169	92.3	32	Q8Q68	Q8Q68 oncorhynch
Q91157	166	90.7	136	Q8Q78	Q8Q78 fugu rubrip
Q91157	159	86.9	32	Q8PS21	Q8PS21 carassius a
Q91157	158	86.3	62	Q79813	Q79813 oncorhynch
Q91157	157	85.8	65	Q9W623	Q9W623 gallus gall
Q91157	156	85.2	50	Q9QYCA	Q9QYCA paralichthy
Q91157	112	61.2	140	Q9NOV5	Q9NOV5 equus caball

ALIGNMENTS

RESULT 1
 ID Q91157 PRELIMINARY; PRT; 56 AA.
 AC Q91157;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Calcitonin (Fragment).
 GN CALC I.
 OS Oncorhynchus gorbuscha (Pink salmon) (Humpback salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8017;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=GILL;
 RX MEDLINE=94255438; PubMed=8197156;
 RA Martini K., Maubras L., Taboulet J., Jullienne A., Berry M.,
 RA Milhaud G., Benson A.A., Moukhtar M.S., Cressent M.;
 RT "The calcitonin gene is expressed in salmon gills";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:4912-4914(1994).
 DR EMBL; X78080; CAA54988.1;
 DR HSSP; P01262; IBLK0.
 DR InterPro; IPR001693; Calcitonin-like.
 DR InterPro; IPR001935; Calcitonin-A.
 DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
 DR PRINTS; PR00270; CALCITONIN.
 DR SMART; SM00113; CALCITONIN; 1.
 DR PROSITE; PS00258; CALCITONIN; 1.
 FT NON_TER 1 34
 FT CHAIN 3 34
 SQ SEQUENCE 56 AA; 6165 MW; B073F85C56C1848F CRC64;
 Query Match 97.3%; Score 178; DB 13; Length 56;
 Best Local Similarity 100.0%; Pred. No. 2.9e-20;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CSNLSCTVGLKLSQELHKLQTYPRNTNGSTGTPG 34

```
DR PRINTS: PR00270; CALCITONIN.
DR SMART: SM00113; CALCITONIN; 1.
DR PROSITE: PS00258; CALCITONIN; 1.
FT NON_TER 1
SQ SEQUENCE 62 AA: 6865 MW: EE8AA50D5ED4CA99 CRC64;

Query Match 97.3%; Score 178; DB 13; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.3e-20;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTGP 34
   |||||||
Db 9 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTGP 41

RESULT 4
Q8QG84 PRELIMINARY; PRT; 32 AA.
ID Q8QG84
AC Q8QG84;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Calcitonin (Fragment).
GN Oncorhynchus gorbuscha (Pink salmon) (Humpback salmon).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8017;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang B.H., Mao Y.X., Wang G.G., Yang G.P., Zhang X.C.;
RT "Cloning and Sequence Analysis of Salmon Calcitonin Genes from Three
   Different Sources.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF491872; AAL99993.1;
FT NON_TER 1 32
FT NON_TER 32 32
SQ SEQUENCE 32 AA: 3435 MW: AFC935519807E7C2 CRC64;

Query Match 94.0%; Score 172; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTGP 33
   |||||||
Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTGP 32

RESULT 5
Q8QG82 PRELIMINARY; PRT; 32 AA.
ID Q8QG82
AC Q8QG82;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Calcitonin (Fragment).
GN CT.
OS Oncorhynchus sp. Fy-02.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=190488;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang B.H., Mao Y.X., Wang G.G., Yang G.P., Zhang X.C.;
RT "Cloning and Sequence Analysis of Salmon Calcitonin Genes from Three
   Different Sources.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF491874; AAL99995.1;
FT NON_TER 1 32
FT NON_TER 32 32
SQ SEQUENCE 32 AA: 3435 MW: AFC935519807E7C2 CRC64;
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Query Match          94.0%; Score 172; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 6
Q8QG73 ID Q8QG73 PRELIMINARY; PRT; 32 AA.
AC Q8QG73;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Calcitonin (Fragment).
GN CT.
OS Oncorhynchus sp. BZ-2002.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=192133;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang B., Mao Y., Wang G., Zhang X.;
RT "Cloning and Sequence Analysis of Salmon Calcitonin Genes of
RT Aquaculture.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF497755; AAM18086.1; -
FT NON_TER 1
FT NON_TER 32
SQ SEQUENCE 32 AA; 3435 MW; AFC935519807E7C2 CRC64;

Query Match          94.0%; Score 172; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 7
Q8QG72 ID Q8QG72 PRELIMINARY; PRT; 32 AA.
AC Q8QG72;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Calcitonin (Fragment).
GN CT.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang B., Mao Y., Wang G., Zhang X.;
RT "Cloning and Sequence Analysis of Salmon Calcitonin Genes of
RT Aquaculture.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF497756; AAM18087.1; -
FT NON_TER 1
FT NON_TER 32
SQ SEQUENCE 32 AA; 3435 MW; AFC935519807E7C2 CRC64;

Query Match          94.0%; Score 172; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 8
Q8QG71 ID Q8QG71 PRELIMINARY; PRT; 32 AA.
AC Q8QG71;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Calcitonin (Fragment).
GN CT.
OS Oncorhynchus kisutch (Coho salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8019;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang B., Mao Y., Wang G., Zhang X.;
RT "Cloning and Sequence Analysis of Salmon Calcitonin Genes of
RT Aquaculture.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF497757; AAM18088.1; -
FT NON_TER 1
FT NON_TER 32
SQ SEQUENCE 32 AA; 3435 MW; AFC935519807E7C2 CRC64;

Query Match          94.0%; Score 172; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 9
Q8QG70 ID Q8QG70 PRELIMINARY; PRT; 32 AA.
AC Q8QG70;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Calcitonin (Fragment).
GN CT.
OS Salvelinus alpinus (Arctic char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8036;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang B., Mao Y., Wang G., Zhang X.;
RT "Cloning and Sequence Analysis of Salmon Calcitonin Genes of
RT Aquaculture.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF497758; AAM18089.1; -
FT NON_TER 1
FT NON_TER 32
SQ SEQUENCE 32 AA; 3435 MW; AFC935519807E7C2 CRC64;

Query Match          94.0%; Score 172; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

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RESULT 10
O8QG83 ID O8QG83 PRELIMINARY; PRT; 32 AA.
AC O8QG83;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Calcitonin (Fragment).
GN CT.
OS Oncorhynchus keta (Chum salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang B.H., Mao Y.X., Wang G.G., Yang G.P., Zhang X.C.;
RT "Cloning and Sequence Analysis of Salmon Calcitonin Genes from Three
  Different Sources.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF491873; AAL99994.1;
FT NON_TER 1
FT NON_TER 32
SQ SEQUENCE 32 AA; 3462 MW; AFC935406807E7C2 CRC64;

Query Match 92.3%; Score 169; DB 13; Length 32;
Best Local Similarity 96.9%; Pred. No. 3.9e-19;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CSNLSTCVLGKLSQELHKLQTYPTNTGNGTP 32

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AC O8QFT8;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Calcitonin.
GN CALC.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Clark M.S.;
RT "Structure and expression of Fugu calcitonin gene.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ309015; CAC81278.1;
FT CHAIN 83
FT CHAIN 114
SQ SEQUENCE 136 AA; 14997 MW; A9A9FA80D3E584E4 CRC64;

Query Match 90.7%; Score 166; DB 13; Length 136;
Best Local Similarity 90.9%; Pred. No. 6.1e-18;
Matches 30; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 CSNLSTCVLGKLSQELHKLQTYPTNTGSGTPG 34
Db 83 CSNLSTCVLGKLSQELHKLQTYPTNTGNGTPG 115

RESULT 12
O9PS21 ID O9PS21 PRELIMINARY; PRT; 32 AA.
AC O9PS21;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

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DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Calcitonin, CT.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE.
RX MEDLINE=93202415; PubMed=8454163;
RA Satsuyama Y., Ukawa K., Kai-ya H., Oguro C., Takei Y., Watanabe T.X.,
RA Nakajima K., Sakakibara S.;
RT "Goldfish calcitonin: purification, characterization, and hypocalcemic
  potency.";
RL Gen. Comp. Endocrinol. 89:189-194 (1993).
DR HSP; P01262; IBKU.
DR InterPro; IPR001693; Calcitonin-like.
DR InterPro; IPR001935; Calcitonin_A.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00270; CALCITONIN_A.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
SQ SEQUENCE 32 AA; 3390 MW; AFC93549F818560F CRC64;

Query Match 86.9%; Score 159; DB 13; Length 32;
Best Local Similarity 90.6%; Pred. No. 1.4e-17;
Matches 29; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 CSNLSTCVLGKLSQELHKLQTYPTNTGSGTP 33
Db 1 CSNLSTCVLGKLSQELHKLQTYPTNTGAGTP 32

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AC P79813;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Calcitonin 4 (Fragment).
OS Oncorhynchus gorbuscha (Pink salmon) (Humpback salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8017;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97057244; PubMed=8901583;
RA Jansz H., Martial K., Zandberg J., Milhaud G., Benson A.A.,
RA Julienne A., Moukhtar M.S., Cressent M.;
RT "Identification of a new calcitonin gene in the salmon Oncorhynchus
  gorbuscha.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:12344-12348 (1996).
DR EMBL; U71286; AAB38532.1;
DR HSP; P01262; IBKU.
DR InterPro; IPR001693; Calcitonin-like.
DR InterPro; IPR001935; Calcitonin_A.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00270; CALCITONIN_A.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
FT NON_TER 1
FT CHAIN 1
FT CHAIN 6
FT CHAIN 9
FT CHAIN 40
FT CHAIN 45
FT CHAIN 62
SQ SEQUENCE 62 AA; 6860 MW; 1316EEB8EACF199 CRC64;

Query Match 86.3%; Score 158; DB 13; Length 62;
Best Local Similarity 84.8%; Pred. No. 4.4e-17;
Matches 28; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 2 CSNLSTCVLGKLSQELHKLQTYPTNTGSGTPG 34

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Db 9 CSNLSTCVLGKLSQDLHKLOTFFRTDVGAGTPG 41

RESULT 14

Q9W6Z3	PRELIMINARY;	PRT;	65 AA.
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AC	Q9W6Z3;		
DT	01-NOV-1999 (TrEMBLrel. 12, Created)		
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)		
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)		
DE	Calcitonin/CGRP gene exon 4.		
DE	Gallus gallus (Chicken).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauaria; Aves; Neognathae; Galliformes; Phasianinae;		
OC	Gallus.		
OC	NCBI_TaxID=9031;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RN	MEDLINE=88030046; PubMed=3666142;		
RX	Minvielle S., Cressent M., Delehaye M.C., Second N., Milhaud G.,		
RA	Jullienne A., Moukhtar M.S., Lasmoules F.;		
RA	"Sequence and expression of the chicken calcitonin.";		
RL	FEBS Lett. 223:63-68(1987).		
RT	EMBL; X06313; CAA29632.1; -.		
DR	HSSP; P01262; 1BKU.		
DR	InterPro; IPR001693; Calcitonin-like.		
DR	InterPro; IPR001935; Calcitonin.A.		
DR	Pfam; PF00214; Calc_CGRP_IAPP; 1.		
DR	PRINTS; PR00270; CALCITONIN.		
DR	SMART; SM00113; CALCITONIN; 1.		
DR	PROSITE; PS00258; CALCITONIN; 1.		
DR	SEQUENCE 65 AA; 7232 MW; 772C54DA8A5ABC0B CRC64;		

RESULT 15

Q90YC4	PRELIMINARY;	PRT;	50 AA.
AD	Q90YC4;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)		
DE	Calcitonin (Fragment).		
DE	CT/CGRP.		
GN	Paralichthys olivaceus (Flounder).		
OS	Paralichthys olivaceus (Flounder).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;		
OC	Pleuronectoidei; Paralichthyidae; Paralichthys.		
OX	NCBI_TaxID=8255;		
RN	[1]		
RY	SEQUENCE FROM N.A.		
RX	MEDJLN-21406117; PubMed-11514025;		
RA	Suzuki N., Suzuki T., Kurokawa T.;		
RT	"Cloning of a calcitonin gene-related peptide from genomic DNA and its		
RT	mRNA expression in flounder, Paralichthys olivaceus.,"		
RL	Peptides 22:1435-1438(2001).		
DR	EMBL; AB052782; BAB64410.1; --		
DR	InterPro; IPR001693; Calcitonin-like.		
DR	Pfam; PF00214; Calc_CGRP_IAPP; 1.		
FT	NON_TER	1	
FT	CHAIN	1	
FT	SEQUENCE	50 AA;	5426 MW; ABD8859A27DA249F CRC64;
SQ			

Best Local Similarity 81.8%; Pred. No. 7.1e-17;
Matches 27; Conservative 4; Mismatches 2

Search completed: May 30, 2003, 09:53:05
Job time : 81 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 09:49:44 ; Search time 14 seconds
(without alignments)
71.456 Million cell updates/sec

Title: SEQ1

Perfect score: 183
Sequence: 1 mcsnlstcvlgklsqelhkltqyprntngsgtpg 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	178	97.3	33	1 US-07-776-272-7
2	172	94.0	32	1 US-07-952-735A-6
3	172	94.0	32	1 US-08-164-408A-6
4	172	94.0	32	1 US-08-164-408A-7
5	172	94.0	32	1 US-07-794-288D-4
6	172	94.0	32	1 US-08-176-153-2
7	172	94.0	32	1 US-08-424-866-4
8	172	94.0	32	1 US-08-477-727A-6
9	172	94.0	32	1 US-08-477-727A-18
10	172	94.0	32	1 US-08-477-727A-31
11	172	94.0	32	1 US-08-477-727A-43
12	172	94.0	32	2 US-08-595-868C-38
13	172	94.0	32	3 US-08-847-007A-2
14	172	94.0	32	3 US-09-071-090-2
15	172	94.0	32	4 US-09-139-819A-38
16	172	94.0	32	4 US-09-750-913-38
17	172	94.0	32	5 PCT-US93-12692-2
18	172	94.0	32	5 PCT-US94-14303-2
19	172	94.0	32	5 PCT-US96-05372-4
20	172	94.0	32	6 5183802-3
21	165	90.2	33	1 US-07-776-272-8
22	163	89.1	32	3 US-08-907-602-1
23	162	88.5	32	4 US-08-467-472C-20
24	162	88.5	32	4 US-09-384-061-20
25	159	86.9	32	1 US-07-952-735A-5
26	159	86.9	32	1 US-08-490-669-3
27	159	86.9	32	1 US-08-424-866-1

28	159	86.9	32	2	US-08-322-386B-2	Sequence 2, Appli
29	159	86.9	32	2	US-08-595-868C-37	Sequence 37, Appli
30	159	86.9	32	3	US-08-847-007A-3	Sequence 3, Appli
31	159	86.9	32	3	US-09-071-090-3	Sequence 37, Appli
32	159	86.9	32	4	US-09-139-819A-37	Sequence 37, Appli
33	159	86.9	32	4	US-09-750-913-37	Sequence 37, Appli
34	159	86.9	32	5	PCT-US96-05372-1	Sequence 1, Appli
35	159	86.9	32	6	5183802-4	Patent No. 5183802
36	158	86.3	32	3	US-08-467-472C-21	Sequence 21, Appli
37	158	86.3	32	4	US-09-384-061-21	Sequence 21, Appli
38	157	85.8	32	4	US-08-595-868C-39	Sequence 39, Appli
39	157	85.8	32	4	US-09-139-819A-39	Sequence 39, Appli
40	157	85.8	32	4	US-09-750-913-39	Sequence 39, Appli
41	157	85.8	33	1	US-07-776-272-9	Sequence 9, Appli
42	155	84.7	31	3	US-08-847-007A-7	Sequence 7, Appli
43	155	84.7	31	3	US-09-071-090-7	Sequence 7, Appli
44	154	84.2	32	2	US-08-595-868C-40	Sequence 40, Appli
45	154	84.2	32	3	US-07-401-432-45	Sequence 45, Appli

ALIGNMENTS

RESULT 1
US-07-776-272-7
; Sequence 7, Application US/07776272
; Patent No. 5612454
; GENERAL INFORMATION:
; APPLICANT: Kaminuma, Toshihiko
; APPLICANT: Iida, Toshi
; APPLICANT: Tajima, Masahiro
; TITLE OF INVENTION: Process for Purification of Polypeptide
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player
; STREET: 1233 20th St. N.W. P.O. Box 18218
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: United States of America
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07/776,272
; APPLICATION NUMBER: 07/776,272
; FILING DATE: 19911129
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P-450-23167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-0400
; TELEFAX: 202-887-0605
; TELEX: 440706
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Salmon
; US-07-776-272-7

Query Match 97.3%; Score 178; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.4e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wigman, Cohen, Leitner, & Myers, P.C.
; STREET: 1735 Jefferson Davis Hwy., Suite 200
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, Kb storage
; COMPUTER: IQ 486
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,408A
; FILING DATE: 09-DEC-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Herbert
; REGISTRATION NUMBER: 25,109
; REFERENCE/DOCKET NUMBER: 3721-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-4300
; TELEFAX: (703)413-8129
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: Ser at position 2 substituted
; OTHER INFORMATION: with tert-butyl
; OTHER INFORMATION: Ser at position 5 substituted with tert-butyl
; OTHER INFORMATION: Tyr at position 4 substituted with tert-butyl
; OTHER INFORMATION: Thr at position 6 substituted with tert-butyl
; OTHER INFORMATION: Thr at position 11 substituted with tert-butyl
; OTHER INFORMATION: Lys at position 13 substituted with tert-butyl
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; OTHER INFORMATION: His at position 18 substituted with t-butoxycarbonyl
; OTHER INFORMATION: Lys at position 21 substituted with tert-butyl
; OTHER INFORMATION: Thr at position 22 substituted with tert-butyl
; OTHER INFORMATION: Tyr at position 24 substituted with
; OTHER INFORMATION: Arg at position 24 substituted with
; OTHER INFORMATION: 2,2,5,7,8-pentamethylchroman-6-sulphonyl
; OTHER INFORMATION: Thr at position 25 substituted with tert-butyl
; OTHER INFORMATION: Thr at position 27 substituted with tert-butyl
; OTHER INFORMATION: Thr at position 29 substituted with tert-butyl
; OTHER INFORMATION: Ser at position 31 substituted with tert-butyl
; OTHER INFORMATION: Thr at position 31 substituted with tert-butyl
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RESULT 4
US-08-164-408A-7
; Sequence 7, Application US/08164408A
; Patent No. 5527881
; GENERAL INFORMATION:
; APPLICANT: Poblet, Marcos C
; APPLICANT: Obols, Berta P.
; APPLICANT: Farres, Gemma J.
; TITLE OF INVENTION: Procedure for Preparing Salmon
; TITLE OF INVENTION: Calcitonin
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:

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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,153
FILING DATE:
CLASSIFICATION: 530

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; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 92-20C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-547-8080 ext 427
; TELEFAX: 206-548-2329
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 32
; OTHER INFORMATION: /label= amidated
; OTHER INFORMATION: /note= "C-terminal Proline residue is amidated."
US-08-176-153-2

Query Match 94.0%; Score 172; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 7
US-08-424-866-4
; Sequence 4, Application US/08424866
; Patent No. 5721207
; GENERAL INFORMATION:
; APPLICANT: NO. 5721207le, John F.
; APPLICANT: Abajian, Henry B.
; TITLE OF INVENTION: Method of Treatment of Pain
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,866
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33878
; REFERENCE/DOCKET NUMBER: 1-95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORGANISM: Salmon
; ORIGINAL SOURCE:
US-08-424-866-4

Query Match 94.0%; Score 172; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 8
US-08-477-727A-6
; Sequence 6, Application US/08477727A
; Patent No. 5739106
; GENERAL INFORMATION:
; APPLICANT: Rink, Timothy
; APPLICANT: Young, Andrew
; APPLICANT: Beeley, Nigel
; APPLICANT: Prickett, Kathryn
; TITLE OF INVENTION: APPETITE REGULATING
; TITLE OF INVENTION: COMPOSITIONS
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: 633 WEST FIFTH STREET, SUITE 4700
; CITY: LOS ANGELES
; STATE: CA
; COUNTRY: USA
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,727A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DUFT, BRADFORD J
; REGISTRATION NUMBER: 32,219
; REFERENCE/DOCKET NUMBER: 214/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-552-8400
; TELEFAX: 619-552-0157
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-477-727A-6

Query Match 94.0%; Score 172; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 9
US-08-477-727A-18
; Sequence 18, Application US/08477727A
; Patent No. 5739106

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Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
US-08-477-727A-6
; Sequence 6, Application US/08477727A
; Patent No. 5739106
; GENERAL INFORMATION:
; APPLICANT: Rink, Timothy
; APPLICANT: Young, Andrew
; APPLICANT: Beeley, Nigel
; APPLICANT: Prickett, Kathryn
; TITLE OF INVENTION: APPETITE REGULATING
; TITLE OF INVENTION: COMPOSITIONS
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: 633 WEST FIFTH STREET, SUITE 4700
; CITY: LOS ANGELES
; STATE: CA
; COUNTRY: USA
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,727A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DUFT, BRADFORD J
; REGISTRATION NUMBER: 32,219
; REFERENCE/DOCKET NUMBER: 214/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-552-8400
; TELEFAX: 619-552-0157
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-477-727A-6

Query Match 94.0%; Score 172; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 9
US-08-477-727A-18
; Sequence 18, Application US/08477727A
; Patent No. 5739106

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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DUFT, BRADFORD J
;; REGISTRATION NUMBER: 32,219
;; REFERENCE/DOCKET NUMBER: 214/005
;; TELEPHONE: 619-552-8400
;; TELEFAX: 619-552-0157
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 43:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 32 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
;; ORIGINAL SOURCE:
;; US-08-477-727A-43
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Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CSNLSCTCVLKGKLSQELHKLQTYPRNTGSGTP 32
;;
RESULT 12
US-08-595-868C-38
; Sequence 38, Application US/08595868C
; Patent No. 5962270
; GENERAL INFORMATION:
; APPLICANT: Wagner, Fred
; APPLICANT: Stout, Jay
; APPLICANT: Henriksen, Dennis
; APPLICANT: Partridge, Bruce
; APPLICANT: Holmquist, Bart
; APPLICANT: Frank, Julie
; TITLE OF INVENTION: RECOMBINANT PREPARATION OF CALCITONIN FRAGMENTS AND US
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5962270west Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595.868C
; FILING DATE: 06-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.590S01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/332-5300
; TELEFAX: 612/332-9081
; TELEX:

;; INFORMATION FOR SEQ ID NO: 38:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 32 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; ORIGINAL SOURCE:
;; US-08-595-868C-38
;;
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Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CSNLSCTCVLKGKLSQELHKLQTYPRNTGSGTP 32
;;
RESULT 13
US-08-847-007A-2
; Sequence 2, Application US/08847007A
; Patent No. 6083480
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Bush, Larry R
; APPLICANT: Pearson, Daniel P
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Radiolabeled Peptides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, Seventh Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847.007A
; FILING DATE: 01-MAY-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6083480nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 97,209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..7
; OTHER INFORMATION: /label= disulfide bond
; OTHER INFORMATION: /note= "A disulfide bond exists between the
; OTHER INFORMATION: two sulfur atoms of the cysteine residues;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 32
; OTHER INFORMATION: /label= Amide

OTHER INFORMATION: /note= "The carboxyl terminus is modified to an amide"
 US-08-847-007A-2

Query Match 94.0%; Score 172; DB 3; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.5e-16;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
 Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 14
 US-09-071-090-2
 ; Sequence 2, Application US/09071090
 ; Patent No. 6086850
 ; GENERAL INFORMATION:
 ; APPLICANT: Dean, Richard T.
 ; APPLICANT: Bush, Larry R.
 ; APPLICANT: Pearson, Daniel A.
 ; APPLICANT: Lister-James, John
 ; TITLE OF INVENTION: CALCITONIN RECEPTOR BINDING REAGENTS
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Diatide, Inc.
 ; STREET: 9 Delta Drive
 ; CITY: Londonderry
 ; STATE: NH
 ; COUNTRY: USA
 ; ZIP: 03053

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/071,090
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/847,007
 FILING DATE: 01-MAY-1997

ATTORNEY/AGENT INFORMATION:
 NAME: McDaniel, Patricia A.
 REGISTRATION NUMBER: 33,194
 REFERENCE/DOCKET NUMBER: DIFI 125.1PCT
 TELEPHONE: (603) 437-8970
 TELEFAX: (603) 437-8977

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 STRANDEDNESS:

TOPOLOGY: both
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: CALCITONIN--SALMON
 FEATURE:
 NAME/KEY: Disulfide-bond
 LOCATION: 1..7
 FEATURE:

NAME/KEY: Modified-site
 LOCATION: 32
 OTHER INFORMATION: /product= "PROLINE 32"
 OTHER INFORMATION: /label= amide
 US-09-071-090-2

Query Match 94.0%; Score 172; DB 3; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.5e-16;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
 Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

RESULT 15
 US-09-139-819A-38
 ; Sequence 38, Application US/09139819A
 ; Patent No. 6251635

GENERAL INFORMATION:
 APPLICANT: WAGNER, Fred W.
 APPLICANT: STOUT, Jay S.
 APPLICANT: HENRIKSEN, Dennis B.
 APPLICANT: PARTRIDGE, Bruce E.
 APPLICANT: HOLMQUIST, Bart
 APPLICANT: FRANK, Julie A.
 TITLE OF INVENTION: RECOMBINANT PREPARATION OF CALCITONIN
 TITLE OF INVENTION: FRAGMENTS AND USE THEREOF IN THE PREPARATION OF CALCITONIN
 TITLE OF INVENTION: AND RELATED ANALOGS
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY & LARDNER
 STREET: 3000 K Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20007-5109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/139,819A
 FILING DATE: 25-AUG-1998
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/595,868
 FILING DATE: 06-FEB-1996

ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 089187/0144
 TELEPHONE: (202) 672-5300
 TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-139-819A-38

Query Match 94.0%; Score 172; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.5e-16;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 33
 Db 1 CSNLSTCVLGKLSQELHKLQTYPRNTGSGTP 32

Search completed: May 30, 2003, 09:51:38
 Job time : 15 secs

